

```

Db 1 MVLRLVLLLSWAGMGOGYNPLNKYIRHREGISTYVDSLHOKHOKRAKRAVSHEDQFL 60
QY 61 RLDFAHGRHFLRMKRDTSLSDEKVEYSNKVLDYDTSHYTGHIYEGESLAMEGLL 120
Db 61 RLDFAHGRHFLRMKRDTSLSDEKVEYSNKVLDYDTSHYTGHIYEGESLAMEGLL 120
QY 121 MEDLKSSRLVYAHFMEPAERIKRTPHSHVYIHEDDINYPKHYGQGCADHSHVE 180
Db 121 DGRFEGFIQTGCGTFYVPAERYIKDRTPHSHVYIHEDDINYPKHYGQGCADHSHVE 180
QY 181 RMKRYOMTGVEEVTOIPOEHAANGPELLRRKRTNSAEKNCTOLYIQDHLFPKYYGTRE 240
Db 181 RMKRYOMTGVEEVTOIPOEHAANGPELLRRKRTNSAEKNCTOLYIQDHLFPKYYGTRE 240
QY 241 AVIAQISSHVKAIDITYOTTFDSGIRNISPMVKRIRINTTADKEDPTNPFPPNIGVEKF 300
Db 241 AVIAQISSHVKAIDITYOTTFDSGIRNISPMVKRIRINTTADKEDPTNPFPPNIGVEKF 300
QY 301 LEINSEONHNDYCLAYVTFDRDQDGLAWYGAPSSSGGICEKSKLYSDGKKSLNT 360
Db 301 LEINSEONHNDYCLAYVTFDRDQDGLAWYGAPSSSGGICEKSKLYSDGKKSLNT 360
QY 361 GITTVOYNGSHVPPKYSHTTFAHEVGHNFSGPHDSGTECTPGESKNLQKENGNYIMYAR 420
Db 361 GITTVOYNGSHVPPKYSHTTFAHEVGHNFSGPHDSGTECTPGESKNLQKENGNYIMYAR 420
QY 421 ATSGDKLNNKESLCSIRNISQVLEKRRNRCFVESGQPTICGNMGVBOGEGDCGYSDQCK 480
Db 421 ATSGDKLNNKESLCSIRNISQVLEKRRNRCFVESGQPTICGNMGVBOGEGDCGYSDQCK 480
QY 481 DECCFANPDEGKCKLKLGKQCSQSPQPCITQACAFKSKSEKCRDSDCARBGTNGT 540
Db 481 DECCFANPDEGKCKLKLGKQCSQSPQPCITQACAFKSKSEKCRDSDCARBGTNGT 540
QY 541 ALCPASDPKPNFDCNRHTOVINCOCAGSICEKYGLEBCTCASSSGKDKELCHVCKM 600
Db 541 ALCPASDPKPNFDCNRHTOVINCOCAGSICEKYGLEBCTCASSSGKDKELCHVCKM 600
QY 601 KMDPSTCASTGSVQWSRHFSGRITTLQPSPCNDFRGYCDVFMRCRLVDADGFLARLKA 660
Db 601 KMDPSTCASTGSVQWSRHFSGRITTLQPSPCNDFRGYCDVFMRCRLVDADGFLARLKA 660
QY 661 IESPELEYENIAEIVAHMAVILMGLALIMLAGFIKISVHTPSSNPKLPKPLPGL 720
Db 661 IESPELEYENIAEIVAHMAVILMGLALIMLAGFIKISVHTPSSNPKLPKPLPGL 720
QY 721 KRRRPPQIQOPORORPRESYOGMHMR 748
Db 721 KRRRPPQIQOPORORPRESYOGMHMR 748

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RL Biochem. J. 317:45-50(1996).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN BRAIN. AT LOWER
CC LEVELS IN KIDNEY, SPLEEN, LUNG AND HEART.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M2C (ZINC
CC METALLOPROTEASE).
CC -1- SIMILARITY: HIGH, IN THE MIDDLE REGION, TO DISINTEGRINS.
DR EMBL: Z21961; CAAT9373.1; -.
DR HSSP: P18619; 1EVL.
DR MEROPS: M12.210; -.
DR InterPro: IPR001762; Disintegrin.
DR InterPro: IPR001590; Reprolysin.
DR InterPro: IPR000130; Zn_Mtpetdse.
DR Pfam: PF00200; disintegrin; 1.
DR Pfam: PF01421; Reprolysin; 1.
DR SMART: SM00050; DISIN; 1.
DR PROSITE: PS00215; ADAM_MERO; 1.
DR PROSITE: PS00214; DISINTEGRIN_2; 1.
DR PROSITE: PS00142; ZINC_PROTEASE; UNKNOWN_1.
KM Integrin; Hydrolase; Metalloprotease; Transmembrane; Zinc; Signal;
KM Glycoprotein.
FT SIGNAL 1 19 POTENTIAL.
FT PROPEP 20 213 POTENTIAL.
FT CHAIN 214 455 METALLOPROTEINASE.
FT CHAIN 456 550 DISINTEGRIN.
FT DOMAIN 20 672 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 673 696 POTENTIAL.
FT DOMAIN 697 748 CYTOPLASMIC (POTENTIAL).
FT ACT_SITE 384 384 BY SIMILARITY (BY SIMILARITY).
FT METAL 383 383 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 387 387 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 393 393 ZINC (CATALYTIC) (BY SIMILARITY).
FT CARBOHYD 267 267 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 278 278 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 439 439 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 551 551 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 748 AA; 84188 MW; 202E29830611F9E1 CRC64;

Query Match 94.2%; Score 3852; DB 6; Length 748;
Best Local Similarity 93.7%; Pred. No. 0;
Matches 701; Conservative 20; Mismatches 27; Indels 0; Gaps 0;

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 1, 2002, 15:11:59 ; Search time 98.78 Seconds

(without alignments)  
1107.630 Million cell updates/sec

Title: US-09-871-388-4

Perfect score: 4090

Sequence: 1 MYLRLVLLILLSMAAGMGCGQ.....IQQPRQRPRSYNGHMRR 748

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: SP archaea:\*  
2: SP bacteria:\*  
3: SP fungi:\*  
4: SP human:\*  
5: SP invertebrate:\*  
6: SP mammal:\*  
7: SP mhc:\*  
8: SP organelle:\*  
9: SP phage:\*  
10: SP plant:\*  
11: SP rodent:\*  
12: SP virus:\*  
13: SP vertebrate:\*  
14: SP unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3959	96.8	748	4	014672
2	3852	94.2	748	6	010741
3	3804.5	93.0	749	11	035598
4	3333.5	81.5	691	4	010742
5	2920	71.4	544	11	010743
6	1452	35.5	1236	5	09VJW9
7	1451	35.5	1236	5	09NKE9
8	1450.5	35.5	1239	5	09A902
9	1350.5	33.0	922	5	046354
10	1345.5	32.9	1537	5	09VA12
11	707	17.3	162	13	042568
12	475	11.6	686	5	09A316
13	409.5	10.0	600	13	09PVK7
14	406	9.9	75	6	077633
15	392.5	9.6	845	11	061072
16	386	9.4	819	4	013443
17	372.5	9.1	814	13	012960
18	365.5	8.9	873	13	042595
19	363	8.9	610	13	09DGB9

20	356	8.7	604	13	09PT48
21	356	8.7	735	11	060411
22	352.5	8.6	620	13	042138
23	349.5	8.5	616	13	030495
24	349.5	8.5	728	4	09B211
25	338.5	8.3	617	13	090499
26	337	8.2	606	13	098UF9
27	334	8.2	920	11	035674
28	333	8.1	609	13	09W6M5
29	329	8.0	419	13	032043
30	327.5	8.0	505	13	073795
31	327.5	8.0	918	4	09H013
32	327.5	8.0	918	4	09B2L5
33	325.5	8.0	609	13	090282
34	322	7.9	1569	5	09VFH0
35	318.5	7.8	829	11	09RIV7
36	318	7.8	857	4	090HP2
37	315.5	7.7	832	4	075077
38	315	7.7	610	13	09Y120
39	311	7.6	549	13	090500
40	310.5	7.6	487	13	092119
41	310.5	7.6	760	11	09D4E4
42	309	7.6	610	13	093523
43	308.5	7.5	903	11	061824
44	307	7.5	739	4	09Y307
45	303.5	7.4	481	13	057413

## ALIGNMENTS

RESULT	ID	PRELIMINARY:	PRT:	748 AA.
014672	014672	014672:		
AC	01-JAN-1998 (TREMBLrel. 05, Created)			
DT	01-JAN-1998 (TREMBLrel. 05, Last sequence update)			
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)			
DE	ADAM10.			
GN	ADAM10.			
OS	homo sapiens (Human).			
OC	Eumaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	SEQUENCE FROM N.A.			
RP	MEDLINE=97450992; PubMed=9305925;			
RX	Rosendahl M.S., Ko S.C., Long D.L., Brewer M.T., Rosenzweig B.,			
RA	Hedl E., Anderson L., Pyle S.M., Moreland J., Meyers M.A., Kohno T.,			
RA	Lyons D., Lichenstein H.S.			
RT	"Identification and characterization of a pro-tumor necrosis factor-			
RT	alpha-processing enzyme from the ADAM family of zinc			
RT	metalloproteases."			
RL	J. Biol. Chem. 272:24588-24593(1997).			
DR	EMBL: AF009615; AAC51766.1; -			
DR	HSSP: P18619; 1FVY.			
DR	InterPro: IPR001762; Distintegrin.			
DR	InterPro: IPR001590; Reprolysin.			
DR	InterPro: IPR00130; Zn_MTPeptidse.			
DR	Pfam: PF00200; disintegrin; 1.			
DR	Pfam: PF01421; Reprolysin; 1.			
DR	SMART: SM00050; DISTRN; 1.			
DR	PROSITE: PS50215; ADAM_MEPRO; 1.			
DR	PROSITE: PS50214; DISINTEGRIN_2; 1.			
DR	PROSITE: PS00142; ZINC_PROTEASE; UNKNOWN_1.			
DR	SEQUENCE 748 AA; 84142 MW; 0881E65B17022A71 CRC64;			
QY	1 MYLRLVLLILLSMAAGMGQYGNPLNKYTRHFGLSYVDSLHQKHQRRAVSHEDPTL 60			

Query Match 96.8%; Score 3959; DB 4; Length 748;  
Best Local Similarity 96.9%; Pred. No. 0;  
Matches 725; Conservative 5; Mismatches 18; Indels 0; Gaps 0;

DR PROSITE: PS50214; DISINTEGRIN\_2; 1.  
 DR PROSITE: PS00142; ZINC\_PROTEASE; UNKNOWN\_1.  
 FT INTEGRIN.  
 FT NON\_TER  
 SQ SEQUENCE 691 AA; 77632 MW; 8B43698F246B292 CRC64;

Query Match 81.5%; Score 3333.5; DB 4; Length 691;  
 Best Local Similarity 88.9%; Pred. No. 8.1e-265;  
 Matches 614; Conservative 7; Mismatches 19; Indels 51; Gaps 1;

QY 109 GEEGSLAMGLIMEDLDSSRLVVAHMFPAEYIYIDRLPFIYSVYHEDDIN-----162  
 DB 1 GEEGSHGVSVDGREGFQIQTGRTVEPAERYIDRLPFIYSVYHEDDIN-----162  
 QY 163 -----YPRKKGPOGCAHDS 177  
 DB 61 LRLMSLELMTSCCLPCALLHSKKAIVNSHCILYFKPMGSELYYHAKKGPOGCAHDS 120  
 QY 178 VFERMRYQMTGVVEVTOIPOEHAANGPELLRRKRTNSAEKMTQOLYIQTDHLFFKYYG 237  
 DB 121 VFERMRYQMTGVVEVTOIPOEHAANGPELLRRKRTNSAEKMTQOLYIQTDHLFFKYYG 180  
 QY -238 TREAVIAQISSHVKAIDITYQTDFSGIRNISFMVKRIRINTADEKDPNPRFPNIGY 237  
 DB 181 TREAVIAQISSHVKAIDITYQTDFSGIRNISFMVKRIRINTADEKDPNPRFPNIGY 240  
 QY 298 EKFELENSQNHDDYCLAVYFTDRDDEGVLGLAWGAPSGSGGICEKSKLSDGKRS 357  
 DB 241 EKFELENSQNHDDYCLAVYFTDRDDEGVLGLAWGAPSGSGGICEKSKLSDGKRS 300  
 QY 358 LNVGITYVQNGSHVPRKSHITFAHEVGNFNSPHDSGTECTPGESKNLQKENGNYIM 417  
 DB 301 LNVGITYVQNGSHVPRKSHITFAHEVGNFNSPHDSGTECTPGESKNLQKENGNYIM 360  
 QY 418 YARATSGDKLNNNKFSICIRNISQVLEKRRNCFVESGPIGNGVVEGEGEDCGYSYD 477  
 DB 361 YARATSGDKLNNNKFSICIRNISQVLEKRRNCFVESGPIGNGVVEGEGEDCGYSYD 420  
 QY 478 QCKDECCFDANQPEGRCKLPGKQCSPPGCTAOCARSKSEKCRDSDCAREGICN 537  
 DB 421 QCKDECCFDANQPEGRCKLPGKQCSPPGCTAOCARSKSEKCRDSDCAREGICN 460  
 QY 538 GFPAALCASPPKRNFTDCNHNTOYCTINGOCAGSICEKYGLEECTCASSDGKDEKELCHVC 597  
 DB 481 GFPAALCASPPKRNFTDCNHNTOYCTINGOCAGSICEKYGLEECTCASSDGKDEKELCHVC 540  
 QY 598 CMKKMDPSTCASTGVSQVMSRHFSGRTITLQPGSPCNDERFGYCVFMRKRLVYDADGLARL 657  
 DB 541 CMKKMDPSTCASTGVSQVMSRHFSGRTITLQPGSPCNDERFGYCVFMRKRLVYDADGLARL 600  
 QY 658 KKAIFSELYENTIAEWIVAHMAVLLMGIALIMLAGFIKICSVHTPPSSNPKLPKPKLP 717  
 DB 601 KKAIFSELYENTIAEWIVAHMAVLLMGIALIMLAGFIKICSVHTPPSSNPKLPKPKLP 660  
 QY 718 GTLKRPRPOPPIOPOROPRESYOMGHMR 748  
 DB 661 GTLKRPRPOPPIOPOROPRESYOMGHMR 691

RESULT 5  
 ID 010743 PRELIMINARY: PRT; 544 AA.  
 AC 010743;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE DISINTEGRIN-METALLOPROTEASE PRECURSOR (EC 3.4.24.-) (METELIN-ASSOCIATED METALLOPROTEINASE) (WADN) (FRAGMENT).  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 NCBI\_Taxid=10116;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;  
 RA MEDLINE=66276398; PubMed=8694785;  
 RX Howard L., Mitchell S., Lu X., Griffiths S., Glynn P.;  
 RT "Molecular cloning of MAM: a catalytically active mammalian  
 RT disintegrin-metalloprotease expressed in various cell types";  
 RL Biochem. J. 317:45-50(1996).  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12 (ZINC  
 CC METALLOPROTEASE); ALSO KNOWN AS THE REPOLYSIN SUBFAMILY.  
 CC -1- SIMILARITY: HIGH, IN THE MIDDLE REGION, TO DISINTEGRINS.  
 DR EMBL: Z48444; CAAB8359.1; -  
 DR HSSP: P18619; 1FV.  
 DR MEROPS: M12.210; -  
 DR InterPro: IPR001762; Disintegrin.  
 DR InterPro: IPR001590; Repolysin.  
 DR InterPro: IPR000130; Zn\_MTPeptide.  
 DR Pfam: PF00200; disintegrin; 1.  
 DR Pfam: PF01421; Repolysin; 1.  
 DR PRINTS: PR00289; DISINTEGRIN.  
 DR SMART: SM00050; DISIN: 1.  
 DR PROSITE: PS50215; ADAM\_MEROPS: 1.  
 DR PROSITE: PS50214; DISINTEGRIN\_2; 1.  
 DR PROSITE: PS00142; ZINC\_PROTEASE; UNKNOWN\_1.  
 DR Integrin: Hydrolase; Metalloprotease; Transmembrane; Zinc; Signal;  
 KM Glycoprotein.  
 FT NON\_TER 1 9  
 FT SIGNAL <1 1  
 FT CHAIN 10 241 METALLOPROTEINASE.  
 FT CHAIN 242 346 DISINTEGRIN.  
 FT DOMAIN 10 468 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 469 492 POTENTIAL.  
 FT DOMAIN 493 544 CYTOPLASMIC (POTENTIAL).  
 FT ACT SITE 180 180 BY SIMILARITY.  
 FT METAL 179 179 ZINC (CATALYTIC) (BY SIMILARITY).  
 FT METAL 183 183 ZINC (CATALYTIC) (BY SIMILARITY).  
 FT METAL 189 189 ZINC (CATALYTIC) (BY SIMILARITY).  
 FT CARBOHYD 63 63 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 74 74 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 235 235 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 347 347 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 544 AA; 60444 MW; F75E0B8D6C8B87DD CRC64;

Query Match 71.4%; Score 2920; DB 11; Length 544;  
 Best Local Similarity 96.9%; Pred. No. 4.7e-231;  
 Matches 527; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY 205 GPELLRKKRTNSAEKMTQOLYIQTDHLFFKYYGTREAVIAQISSHVKAIDITYQTDFSG 264  
 DB 1 GPELLRKKRTTLPERNVTCOLYIQTDHLFFKYSYGTREAVIAQISSHVKAIDITYQTDFSG 60  
 QY 265 INISFMVKRIRINTADEKDPNPRFPNIGVEKFELENSQNHDDYCLAVYFTDRD 324  
 DB 61 INISFMVKRIRINTADEKDPNPRFPNIGVEKFELENSQNHDDYCLAVYFTDRD 120  
 QY 325 DGVGLAWGAPSGSGGICEKSKLYSDGKKSMTGIIYVQNGSHVPRKSHITFAHE 384  
 DB 121 DGVGLAWGAPSGSGGICEKSKLYSDGKKSMTGIIYVQNGSHVPRKSHITFAHE 180  
 QY 385 VGHNFSGPHDSGTECTPGESKNLQKENGNYIMVYARATSGDKLNNNKFSICIRNISQVL 444  
 DB 181 VGHNFSGPHDSGTECTPGESKNLQKENGNYIMVYARATSGDKLNNNKFSICIRNISQVL 240  
 QY 445 EKKRRNCFVESGPIGNGVVEGEGEDCGYSYDQCKDECCFDANQPEGRCKLPGKQCS 504  
 DB 241 EKKRRNCFVESGPIGNGVVEGEGEDCGYSYDQCKDECCFDANQPEGRCKLPGKQCS 300  
 QY 505 PQGPGCTAOCARSKSEKCRDSDCAREGICNGTALCPASDPKPNFTDCNRHTQVCIN 564  
 DB 301 PQGPGCTAOCARSKSEKCRDSDCAREGICNGTALCPASDPKPNFTDCNRHTQVCIN 360

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Db 421 ATSGDKLNKNNKFSLSIRINISQVLEKRRNCFVESGQPIGNGVDEGEEDCGYSDQC 480
QY 481 DECCFDANQPEGRKCKLPKQKQSPSGPCTAOCAPKSKSEKCRDSDCAREGICNGFT 540
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 481 DECCFDANQPEGRKCKLPKQKQSPSGPCTAOCAPKSKSEKCRDSDCAREGICNGIT 540
QY 541 ALCPASPRKPNFTDCNHNTOVCINGOCAGSICEKHGLEECTCASSDGKDKELCHVCCM 600
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 541 ALCPASPRKPNFTDCNHNTOVCINGOCAGSICEKHGLEECTCASSDGKDKELCHVCCM 600
QY 601 KMPDSTCASTGVSQVMSRHFSGRTITLQPSPCNDPFGCDVFMKRCRLVDADGFLARLKA 660
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 601 KMPDSTCASTGVSQVMSRHFSGRTITLQPSPCNDPFGCDVFMKRCRLVDADGFLARLKA 660
QY 661 IFSELEYENIAEWIVAHMAVLLMGIALIMLAGFIKICSVHTPSSNPKLPPLPGLT 720
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 661 IFSELEYENIAEWIVAHMAVLLMGIALIMLAGFIKICSVHTPSSNPKLPPLPGLT 720
QY 721 KRRRPPQIOPQOROPRPRESTYOMGHMR 748
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 721 KRRRPPQIOPQOROPRPRESTYOMGHMR 748

RESULT 3
035598 PRELIMINARY; PRT: 749 AA.
AC 035598;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE KIZBANIAN.
GN ADAM10 OR MKU2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97386452; PubMed=9244301;
RA Pan D., Rubin G.M.;
RT "Kuzbanian controls proteolytic processing of Notch and mediates
RT lateral inhibition during Drosophila and vertebrate neurogenesis.";
RL Cell 90:271-280(1997).
DR EMBL: AF011379; AAC53303.1; -.
DR HSSP: P18619; 1FVL.
DR MEROPS: M12.211; -.
DR MGD: MGI:109548; Adam10.
DR InterPro: IPR001762; Disintegrin.
DR InterPro: IPR001590; Repolysin.
DR InterPro: IPR000130; Zn_MTPeptide.
DR Pfam: PF00200; disintegrin; 1.
DR Pfam: PF01421; Repolysin; 1.
DR SMART: SM00050; DISIN: 1.
DR PROSITE: PS50215; ADAM_MERPO: 1.
DR PROSITE: PS50214; DISINTEGRIN_2: 1.
DR PROSITE: PS00142; ZINC_PROTEASE: UNKNOWN: 1.
SQ SEQUENCE 749 AA: 83966 MW: 06CEC3EB2C5F4F94 CRC64;

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Db 121 DGRFEGFITRGTFYIEPAERYIKDRILPFHSVYIHEDDIYPRHKYGGSCADHSVFE 180
QY 181 RMKRYOMTVEEYVTOIPEEHA-NGDELLRRKRINSKNTCOLYIOTDILFFYYGTR 239
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 RMKRYOMTVEEYVTOIPEEHA-NGDELLRRKRINSKNTCOLYIOTDILFFYYGTR 240
QY 240 EAVIAOISSHVAIDITYOTDPSGIRNISPWKRRIRITMTADEKDPNPFPPNIGEK 299
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 EAVIAOISSHVAIDITYOTDPSGIRNISPWKRRIRITMTADEKDPNPFPPNIGEK 300
QY 300 FLELNEQNHDDYCLAYVFTDRDFDGVGLAMVGAPESSSGGICEKSKLYSDGKKSLN 359
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 FLELNEQNHDDYCLAYVFTDRDFDGVGLAMVGAPESSSGGICEKSKLYSDGKKSLN 360
QY 360 TGIITVQNTGSHVPPKVSHTTFAHEYGHFSGPHDSGTCTGCEKSKNLQKENGNTYMA 419
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 361 TGIITVQNTGSHVPPKVSHTTFAHEYGHFSGPHDSGTCTGCEKSKNLQKENGNTYMA 420
QY 420 RATSGDKLNKNNKFSLSIRINISQVLEKRRNCFVESGQPIGNGVDEGEEDCGYSDQC 479
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 421 RATSGDKLNKNNKFSLSIRINISQVLEKRRNCFVESGQPIGNGVDEGEEDCGYSDQC 480
QY 480 KDECDFDANQPEGRKCKLPKQKQSPSGPCTAOCAPKSKSEKCRDSDCAREGICNGF 539
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 481 KDECDFDANQPEGRKCKLPKQKQSPSGPCTAOCAPKSKSEKCRDSDCAREGICNGF 540
QY 540 TALCPASDRKPNFTDCNHNTOVCINGOCAGSICEKHGLEECTCASSDGKDKELCHVCCM 599
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 541 TALCPASDRKPNFTDCNHNTOVCINGOCAGSICEKHGLEECTCASSDGKDKELCHVCCM 600
QY 600 KMPDSTCASTGVSQVMSRHFSGRTITLQPSPCNDPFGCDVFMKRCRLVDADGFLARLKA 659
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 601 KMPDSTCASTGVSQVMSRHFSGRTITLQPSPCNDPFGCDVFMKRCRLVDADGFLARLKA 660
QY 660 AIFSELEYENIAEWIVAHMAVLLMGIALIMLAGFIKICSVHTPSSNPKLPPLPGLT 719
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 661 AIFSELEYENIAEWIVAHMAVLLMGIALIMLAGFIKICSVHTPSSNPKLPPLPGLT 720
QY 720 LKRRPPQIOPQOROPRPRESTYOMGHMR 748
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 721 LKRRPPQIOPQOROPRPRESTYOMGHMR 749

RESULT 4
010742 PRELIMINARY; PRT: 691 AA.
AC 010742; Q92650;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE DISINTEGRIN-METALLOPROTEASE MADM (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96276398; PubMed=8694785;
RA Howard L., Lu X., Mitchell S., Griffiths S., Glynn P.;
RT "Molecular cloning of MADM: a catalytically active mammalian
RT disintegrin-metalloprotease expressed in various cell types.";
RL Biochem. J. 317:45-50(1996).
DR EMBL: Z48579; CAA88463.1; -.
DR HSSP: P18619; 1FVL.
DR MEROPS: M12.210; -.
DR InterPro: IPR001762; Disintegrin.
DR InterPro: IPR001590; Repolysin.
DR InterPro: IPR000130; Zn_MTPeptide.
DR Pfam: PF00200; disintegrin; 1.
DR Pfam: PF01421; Repolysin; 1.
DR PRINTS: PR00289; DISINTEGRIN.
DR SMART: SM00050; DISIN: 1.
DR PROSITE: PS50215; ADAM_MERPO: 1.

```

OY	565	GQCAAGTCACKEKXGEECCGCASSDCKDKRELCCHVCMCKMMPSTASGVSYVMRSHPGRTI	624
Dd	361	GQCAAGTCACKEKXDEECCTCASSDCKDKRELCCHVCMCKMMPSTASGVSYVMRSHPGRTI	420
OY	625	TLAGSPCPCNDPFRGCVDFEMCRCLTVDAADGPRLARKKAIFSPBELYEIAEWIVAHMMVAVLIM	684
Dd	421	TLAGSPCPCNDPFRGCVDFEMCRCLTVDAADGPRLARKKAIFSPOLYEIAEWIVAHMMVAVLIM	480
OY	685	GIALIMTMAGFIKICSVHTTSSNPKLPPPKPLDPGLTKRRRPPPIODOPORPRPRESYONG	744
Dd	481	GIALIMTMAGFIKICSVHTTSSNPKLPPPKPLDPGLTKRRRPPPIODOPORPRPRESYONG	540
OY	745	HMRH	748
Dd	541	HMRH	544
RESULT	6		
OYJW9		PRELIMINARY;	PRT; 1238 AA.
ID	OYJW9		
DT	01-MAY-2000 (TEMBUREl. 13, Created)		
DT	01-MAY-2000 (TEMBUREl. 13, Last sequence update)		
DT	01-JUN-2001 (TEMBUREl. 17, Last annotation update)		
DE	KUZ PROTEIN		
CN	KUZ OR BG:DS07660.3 OR CG7147.		
OS	Drosophila melanogaster (Fruit fly).		
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;		
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;		
OC	Ephydroidea; Drosophilidae; Drosophila.		
OX	NCHI_TaxID=7227;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-BERKELEY.		
RC	MEDLINE-20196006; Pubmed-10731132;		
RA	Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Goebye J.D.,		
RA	Ananatlides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,		
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,		
RA	Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,		
RA	Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,		
RA	Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,		
RA	Abplil J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,		
RA	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu U., Beasley E.M.,		
RA	Besson K.Y., Benos P.V., Bertman B.P., Bhandari D., Bolshakov S.,		
RA	Botkova D., Botchan M.R., Bouck H., Brokstein P., Brotlier P.,		
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,		
RA	Cherry J.M., CWley S., Dahlke C., Davenport L.B., Davies P.,		
RA	de Pablos B., Delcher A., Deng Z., Deyas A.D., Dew I., Dietz S.M.,		
RA	Dooson K., Doup L.B., Downes M., Duggan-Rocha S., Dunkov B.C., Dunn P.,		
RA	Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,		
RA	Foster C., Gabriellan A.E., Gary N.S., Gelbart W.M., Glasser K.,		
RA	Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,		
RA	Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,		
RA	Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,		
RA	Jatall M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kelchum K.A.,		
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,		
RA	Liao P., Lei Y., Levitsky A.A., Li J., Li Z., Lynch Y., Lin X.,		
RA	Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,		
RA	Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,		
RA	Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,		
RA	Nelson D.R., Nelson K.A., Nixon K., Nusslein D.R., Paley J.M.,		
RA	Palazzo M., Pittman G.S., Pan S., Pollard J., Pull V., Reese M.G.,		
RA	Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,		
RA	Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,		
RA	Spieler E., Spreading A.C., Stapleton M., Strong R., Sun E.,		
RA	Syrkstas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,		
RA	Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,		
RA	Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,		
RA	Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,		
RA	Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,		
RA	Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,		
RT	"The genome sequence of Drosophila melanogaster."		
RL	Science 287:2185-2195(2000).		

OY 614 QMSHESGRTITLQPSPCDNDFGCVDFMRCRLVADGFLARLKAIFSPELYENIAEW 673  
 DB 846 ADKNICKGSIQPSGSPCNFGYCVDFLCKRAVADGFLRLKRLNLLKRLKLTQVAVW 905  
 OY 674 IVAHMAVLLMGTALMLMGFIKISVHTPSSNPKLPPLPGLTKRRPQIPQOP 733  
 DB 906 IVDWMLVLMGVAFIVMGSIKCAVHTPSSNPKRRARRISLTL--RAPMNTLRMO 963  
 OY 734 R---OR-----PRESYOMGHMR 748  
 DB 964 RHPNRCAGPRISIPRAHEAHSR 988  
 RESULT 7  
 Q9NKF9 PRELIMINARY: PRT: 1236 AA.  
 AC Q9NKF9: 01-OCT-2000 (Tremblrel. 15, Created)  
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
 DE KUZ PROTEIN.  
 GN KUZ OR BG:DS07660.3 OR CG147.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Y, CN BW SP;  
 RX MEDLINE=99403001; PubMed=10471707;  
 RA Ashburner M., Mista S., Roote J., Lewis S.E., Blazer R., Davis T.,  
 Doyle C., Galle R., George R., Harris N., Hartzell G., Harvey D.,  
 Hong L., Houston K., Hoskins R., Johnson R., Martin C., Moshrefi A.,  
 Palazzo M., Reese M.G., Spradling A., Tsang G., Wan K., Whiteley K.,  
 Zelniker S., Rubin G.M.,  
 RA "An exploration of the sequence of a 2.9-Mb region of the genome of  
 RT Drosophila melanogaster: the Adh region."  
 RL Genetics 153:179-219(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Y, CN BW SP;  
 RA Zelniker S.E., Ashdani A., Arcalua T.T., Baxter E., Blazer R.G.,  
 Butenhot C., Champe M., Chavez C., Chew M., Ciesiolka L., Doyle C.M.,  
 RA Farlin D.E., Galle R., George R.A., Harris N.L., Hoskins R.A.,  
 RA Houston K.A., Hummel S.R., Kaira K., Kearney L., Kim E., Lee B.,  
 RA Lewis S., Li P., Lomoth M.A., Mazda P., Moshrefi A.R., Moshrefi M.,  
 Nixon K., Paclet J.M., Park S., Pfeiffer B., Poon L., Sequeira A.,  
 RA Sethi H., Solt E., Svirskas R.R., Wan K.H., Weinburg T., Zhang R.,  
 Zieran L.L., Rubin G.M.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RX EMBL: AEO03407; AAF44800.1;  
 DR FLYBASE: FBgn0015954; Kuz.  
 DR InterPro: IPR001762; Disintegrin.  
 DR InterPro: IPR001590; Reprolysin.  
 DR InterPro: IPR001130; Zn\_MTPetase.  
 DR SMART: SM00050; ADAM\_MEPRO: 1.  
 DR PROSITE: PS02015; DISINTEGRIN\_2: 1.  
 DR PROSITE: PS00214; DISINTEGRIN\_2: 1.  
 DR PROSITE: PS00142; ZINC\_PROTEASE; UNKNOWN: 1.  
 SQ SQUENCE 1236 AA: 136343 MW: 40461ACT17040C9AD CRC64:

Query Match 35.5%; Score 1451; DB 5; Length 1236;  
 Best Local Similarity 34.3%; Pred. No. 4,2e-110;  
 Matches 331; Conservative 124; Mismatches 256; Indels 254; Gaps 23;

OY 25 LAKRYHEGLSYNDLQKQARARAVSHEDQFLRDLFHAGRFNLMKRDTSLSFD 84  
 DB 35 LNEYSHYETLNDHEHGRASHNRARSVT-KQGVHLKFKASHGRDFHLRLKDLMTFSN 93  
 OY 85 EFVEVSNKVLVDYDTSHYTGHTGHEGSLAMGL----- 119

DB 94 KIDFYDSKPIDVSTDHIVEGEVIGDRNSYVSGSIHNGVEFGKITTERDAYVEHAKHYF 153  
 OY 120 ----- 119  
 DB 154 PINKRATTTTPSTSTTSATTTATKSTOPTRLAKSNTSTTAVNSKTEFPIKIANSTTS 213  
 OY 120 --LMEDLKDSRLVVAHFMEPAERYIKDR-----TLFHSVLY--HEDDIYPPHY 167  
 DB 214 QQLPEYTESSSSTTTT---FPPTTEYFEDEKERNADELDIFSIITKSHVEDAVENRE 270  
 OY 168 GPOGGA-DHAFPERKAKTQMTVEVYQ-----IPOEHAANGP-- 206  
 DB 271 GHVAGGIGTDEVSSQWMENTIONSVELEPEPMKDYOKLHKQLHKKAPQOQOOPPRK 330  
 OY 207 -----ELLRKRTNSA 217  
 DB 331 YISGDEDFPYPRQKTKEANFAEGAFYDPSTGRRLGSSANVADHQLVHERRRATDGA 390  
 OY 218 -----EKNTOQLYIOTDHLFFKY-----GTREAVIAQ 245  
 DB 391 GDRSGSGSGRGRDRKKNKCSLYIOTDPLIRHIREGIADHGRKYEDEKTRREITS 450  
 OY 246 ISSHYAIDTITQTDPSG---IRNISFVKRIRINTA---DEKDPNPRFPNIGVE 298  
 DB 451 IAHVAVVAVYIRNTRFDRTEHRNIREVQRIKIDDSACRNSYNGPHMFCNEHMDVS 510  
 OY 299 KFELENSQNHDDYCLAYFTDRDQGVGLAWYAGAPSGSGSICKSKLYSD----- 352  
 DB 511 NFLNLHSLDEHDFCLAYFTYRDFTGGTLGLAWASAGAGGICERKTYTTEVGGQY 570  
 OY 353 -GKRSLSLNTGIIIVYNGSHVPPKVSHTTFAHEVGNHNGSPHDSGTECTPGEBSKNLQKE 411  
 DB 571 GKRSLSLNTGIIIVYNGSHVPPKVSHTTFAHEVGNHNGSPHDSGTECTPGEBSKNLQKE 411  
 OY 412 NGNYIMYATATSGDKLNNKFSCLSTRINSOYLE---KKNRCVBSGQPLCGNGVYQ 467  
 DB 624 NGNYIMYATATSGDKLNNKFSCLSTRINSOYLE---KKNRCVBSGQPLCGNGVYQ 467  
 OY 468 GECDGYS-DOCKDECCP-----DANPEGRKCKLPKQCSPOGPGCTA-QCAF 517  
 DB 684 GECDGYS-DOCKDECCP-----DANPEGRKCKLPKQCSPOGPGCTA-QCAF 517  
 OY 518 --KSSSEKCRDSDCAREGICNGFTALCPASDPKPNFTDCNHRVQICNGCAGSICBY 575  
 DB 744 VPTSYHOKKEETECSSWSSTGNTAECEPRHRDXTMCNNGTALCIRGECSSGPLLM 803  
 OY 576 GLEEC--TCASSGDKMDELCHVCCMKMDPSTCASSTGVSQMSRHFSGRTITLQPSPCN 633  
 DB 804 NMKCPSTSTLPHVSKRKLCDLACQDGNSTCRSTSEFADKYNIQKGSISLQPSPCD 863  
 OY 634 DFGYCDVFMRCRLVADGFLARLKAIFSPELYENIAEWIVAHHMAVLLMGTALMLMA 693  
 DB 864 IFQYGVCDVFLKRAVADGFLRLKRLNLLKRLKLTQVAVWLVLMGVAFIVMG 923  
 OY 694 GTIKCSVHTPSSNPKLPPLPGLTKRRPQIPQOPR---OR-----PRESYOM 743  
 DB 924 SEIKCAVHTPSSNPKRRARRISLTL--RAPMNTLRMRHPNRCAGPRISIPRAHEA 981  
 OY 744 GHMR 748  
 DB 982 QHYSR 986  
 RESULT 8  
 Q94902 PRELIMINARY: PRT: 1239 AA.  
 AC Q94902: 01-FEB-1997 (Tremblrel. 02, Created)  
 DT 01-FEB-1997 (Tremblrel. 02, Last sequence update)  
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
 DE KUZBANIAN.  
 GN KUZ OR BG:DS07660.3 OR CG147.  
 OS Drosophila melanogaster (Fruit fly).









DR InterPro: IPR000130; Zn\_MTPeptide.  
 DR SMART: SM00050; DISIN; 1.  
 DR PROSITE: PS50215; ADAM\_MERPRO; 1.  
 DR PROSITE: PS50214; DISINTEGRIN\_2; 1.  
 DR PROSITE: PS00142; ZINC\_PROTEASE; UNKNOWN\_1.  
 KW Protease; Metalloprotease.  
 SQ SEQUENCE 686 AA; 77298 MW; 66D58008A207AE49 CRC64;

Query Match 11.6%; Score 475; DB 5; Length 686;  
 Best Local Similarity 24.8%; Pred. No. 2e-30; Indels 184; Gaps 37;  
 Matches 179; Conservative 100; Mismatches 259;

69 RHFNLMKMDTSLFSDDEFVETSNKVLADYDTSHTYGHITGHEGSLAMGLMEDLK--- 125  
 28 RHAFIRFQSTQSVHFEFLDQEVVDLEPHN-STFH-----ENKVT 71  
 126 -DSSRLVAHFMFEPAERYIKDRTL-----FHSVIYHEDDI-----NYPH 165  
 72 QDGPQIV-----PRDEYIGTVREPRAGRAVLTOLEENVYIGSLYFVDDTLHLEPSYPH 124  
 166 K-----YGPQGGCASHV-----FERMKYQMTGVEVYQIQDEEHAANG 205  
 125 QUSDDLGPAVGVFESDLNLDLSAMPVBNQVSFRANPFLKH--RRATAPSD----- 176  
 206 PELLRKRTNSAEKNTCOLYIQTDLHLEFKYGTREAVIAQ--ISSHVKADITY----- 257  
 177 ----RKQDVANKRNKCTKLAVADYSFISFGKNTGITYTKFLVNIAVNEIYTPIND 232  
 258 --QTTDFSG--IRNISFVAKRIRINTTADEKOPTNPRFPNI-GVEKFL-ELNSEQND 310  
 233 VGEKEDDISGRHFGQNGFEIKELKYLDRPNASD-SHYSYSRIWEVERLLREFAPAEGRK 291  
 311 DYCIAVFDPRDD--GVGLAMVGAAP--SGSSGICEKSKLYSDGKKSLMTGIT--V 365  
 292 DCLVHLVARTFREVAITGLAVYSKKWDETAGGICSGOETP-NGRAVINVLSTFSA 350  
 366 QNYGSHV--PKVSHITFAHEVGHNGSPHD-----SGTECPGGEKSLGQKENGNY 415  
 351 NSRQSTYPLITKEIDIVSHHEGHANGATHDPTIDSDDEVEGESPND-----QNGCKY 404  
 416 IMAARTSGDKLNNKFSICSTRINSQVLEKRNCFVSGQPIGNGNAGEDEDCGY 475  
 405 LMSQYAKQKYDANNVLFSPCSRKLIRDLVILGWESCFQEMTSECGNIGVEDEGCDNGV 464  
 476 SPQCKECCFDANQPEGRCKLKPCKQSPSQPCTACAFKSKSEK--RDDSDCAR 533  
 465 DTDNENCC-----DKCRILAVGAKCSPLNHICTPTFCQHNSTHYCLLPQDSLCKRAD 517  
 534 GICNGFTALCPASDPKPNFTDCNRHTQVINGOCAGSICER--YGLEECTCASSDGDCKD 591  
 518 AVNGSGSGCPSPAPVPDQOECLGEGE-CLNGVCL-PFCEKMSIGKKSIC-----EDL 569  
 592 EL-CHVCKAKKMDPSTCASTGSVONSRHFSGRITLQPSPCNDPFGYCDVPMRCLVYA 650  
 570 ELSRCILCC--RDYNGTCAVPG-----HYLRDVGRC--KGS----- 604  
 651 DGLRLKRAIFSELYEN-----IAEWIAHMAVAVLMGLIALIMLAGFI 696  
 605 ----RDKCY--NEVVDVNRNTELTPTGTGVELEFIKH--IYVIALIFTLIFVGLI 655  
 697 KI 698  
 656 KI 657

RESULT 13  
 Q9PVK7 PRELIMINARY; PRT; 600 AA.  
 AC Q9PVK7  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

DE COBRIN PRECURSOR.  
 OS Naja naja (Indian cobra).  
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Elapidae; Elapinae; Naja.  
 CX NCBI\_TaxID=35670;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=KAUTHIA; TISSUE=VENOM GLAND;  
 RA Bamba B., Bredehorst R., Vogel C.-W.;  
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF063190; AAF00693.1; -.  
 DR HSSP: P17494; 1KST.  
 DR InterPro: IPR001762; Disintegrin.  
 DR InterPro: IPR002870; Pep\_M12B\_propep.  
 DR InterPro: IPR001590; Repolysin.  
 DR InterPro: IPR000130; Zn\_MTPeptide.  
 DR Pfam: PF00200; disintegrin; 1.  
 DR Pfam: PF01562; Pep\_M12B\_propep; 1.  
 DR Pfam: PF01421; Repolysin; 1.  
 DR PRINTS: PR00289; DISINTEGRIN.  
 DR ProDom: PD000664; disintegrin; 1.  
 DR SMART: SM00050; DISIN; 1.  
 DR PROSITE: PS50215; ADAM\_MERPRO; 1.  
 DR PROSITE: PS50214; DISINTEGRIN\_2; 1.  
 DR PROSITE: PS00142; ZINC\_PROTEASE; UNKNOWN\_1.  
 KW Signal.  
 FT SIGNAL 1 6 POTENTIAL.  
 FT CHAIN 180 600 COBRIN.  
 SQ SEQUENCE 600 AA; 67661 MW; C7CD045EBC694290 CRC64;

Query Match 10.0%; Score 409.5; DB 13; Length 600;  
 Best Local Similarity 24.1%; Pred. No. 4e-25;  
 Matches 158; Conservative 90; Mismatches 234; Indels 173; Gaps 30;

47 QAKRAVSHEDQFLRDLFPAHGRHFNLMKMDTSLFSDF-----KVESNKVLD 96  
 36 QNPQPEYKEDT-MQYEQVNGEPVVLHLERNKGLFSDYETETHPADGREITTSPPVD 94  
 97 YDTSHTYGHITGHEGSLAMGLMEDLKSSRLVAHFMFEPAERYIKDRTLPHSVIY 156  
 95 H---CYHGYFQNEADSSAV-ISACDGLKGFKLQGETIFTEP-----LKISDSAHAIY- 145  
 157 HEDDINYPHKYPOGGCASHSVFERMKRYQMTGVEEVN-----QIPDEHANGPELLRK 211  
 146 -----KDNVWEEDETPKICGVTDJTWESDEPLKTSLLTNPPE--Q 185  
 212 KRTNSAEKNTCOLYIQTDLHLEFKYGTREAVI-AOISSHVKADITYQTTDFSGIRNISF 270  
 186 DRYLOAEK-YLEFYVAVVINIMRHKKRQOLVKKRYEMIMTMIVRLNF---HIAL 240  
 271 MYKRI-----RLNTADEKDPNPRFPNIGVEKFLNSEQNDHDDCLAVFTDRPDD 325  
 241 IGLEIWSINELINOSDVKATLDF-----GEWRKRLPKRRDN--KQLLTGIDPFG 292  
 326 GVLGLAMVGAAPSGSGGICEKSKLYSDGKKSLMTGITLYONYSHPVPPKSHITFAHEV 385  
 293 TPVGLAYIGS-----ICNP-----KTSAAVVDYDYSKST--RMVALTMHEM 331  
 386 GHNFGSPHDSGTECTPGESKSLGQKENGNYIMYARANSGLKLNKNSLCSIRINSQVLE 445  
 332 GHNLGMNHDKGF-CTCGFNK-----CYMSTRRTK----PAYQSSCSVRHQRRL 377  
 446 KRRNCFVES-----GQPIGNGMVGEGECQCGYSDQCKDCCFPDANPBERKCKL 498  
 378 RDRPQCIILNKPLSTDIYVPPICGNTFVEVGECQDGPADQSAACC-----NATTKLQ 431  
 499 PKQCSPSQGPCTACAFKSKSEK--RDSDCAREGICNGFTALCPASDPKPNFTDNR 557  
 432 HEAQDSDSE---CEKCKFKGAGAECAKADKDCDLPCLCTGQSAECPTDVRNGRLGC-Q 487  
 558 HTQVCINQCC-----AGSICEKYGLEECTCASSD 586

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DB 488 NNGCYTNGKCPMTNOCIALRGPKVSRDSCFTLNQRTGCGLCRMETG-RKIPCAAKD 546
QY 587 GKDELCHV-----CCMKKMDPSTCAGSYGVOMSRHFGSRTITTLQPGSPCND 634
DB 547 VACGRLFCRKRSMTCNCSISPRDP-----SYGMV-----EPGTRCGD 584

RESULT 14
077633 PRELIMINARY: PRT: 75 AA.
ID 077633:
AC 077633:
DT 01-NOV-1998 (TREMBLREL. 08, Created)
DT 01-NOV-1998 (TREMBLREL. 08, Last sequence update)
DT 01-JUN-2001 (TREMBLREL. 17, Last annotation update)
DE DISINTEGRIN-METALLOPROTEINASE PRECURSOR (FRAGMENT).
GN ADAM-10.
OS Mus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Flannery C.R., Little C.B., Caterson B., Hughes C.E.;
RT "Expression of articular cartilage metalloproteinases by chondrocytes
in fresh tissue and explant, monolayer and agarose cultures.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF069645; AAC23529.1; -.
DR MEROPS; M12.210; -.
DR Interpro: IPR001590; Reprolysin.
DR PROSITE; PS50215; ADAM_MERPRO; 1.
KW Integrin.
FT NON_TER 1 1
FT NON_TER 75 75
SQ SEQUENCE 75 AA: 8224 MW: C03H70C9O1333557 CRC64;

Query Match 9.9%; Score 406; DB 6; Length 75;
Best Local Similarity 100.0%; Pred. No. 4.6e-26;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 392 PHDSECTPGESKNLGGKNGNTIMYARATSGDKLNKNSFSLISIRISQVLEKKRRNC 451
DB 1 PHDSECTPGESKNLGGKNGNTIMYARATSGDKLNKNSFSLISIRISQVLEKKRRNC 60
QY 452 FVESGPGICNGMVE 466
DB 61 FVESGPGICNGMVE 75

RESULT 15
061072 PRELIMINARY: PRT: 845 AA.
ID 061072:
AC 061072: 060618; 061853;
DT 01-JUL-1997 (TREMBLREL. 04, Created)
DT 01-JUL-1997 (TREMBLREL. 04, Last sequence update)
DT 01-JUN-2001 (TREMBLREL. 17, Last annotation update)
DE CELLULAR DISINTEGRIN-RELATED PROTEIN PRECURSOR (MELTRIN GAMMA).
GN ADAM9 OR MLTNG OR MDC9.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Tissue-LUNG;
RC MEDLINE-96178079; Pubmed-8647900;
RA Weskamp G., Kraetzschmar J.R., Reid M., Blobel C.P.;
RT "MDC9, a widely expressed cellular disintegrin containing cytoplasmic
SH3 ligand domains.";
RL J. Cell Biol. 132:717-726(1996).
RN [2]
RP SEQUENCE OF 426-575 FROM N.A.

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RX MEDLINE-96026308; Pubmed-7566181;
RA Yagami-Hironaka T., Sato T., Kurisaki T., Kamijo K., Nabeshima Y.,
RA Fujisawa-Sehara A.;
RT "A metalloprotease-disintegrin participating in myoblast fusion.";
RL Nature 377:652-656(1995).
RN [3]
RP SEQUENCE OF 432-478 FROM N.A.
RC STRAIN-BALB/C;
RX MEDLINE-94195820; Pubmed-8146185;
RA Weskamp G., Blobel C.P.;
RT "A family of cellular proteins related to snake venom disintegrins.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:2748-2751(1994).
CC -1- FUNCTION: MAY MEDIATE CELL-CELL OR CELL-MATRIX INTERACTIONS.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED.
CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
DR EMBL; U06145; AAA18424.1; -.
DR EMBL; U41765; AAC52446.1; -.
DR EMBL; D50412; BAA08913.1; -.
DR HSSP; P18619; 1FVL.
DR MEROPS; M12.209; -.
DR MGD; MGI:105376; Adam9.
DR Interpro: IPR001762; Disintegrin.
DR Interpro: IPR000561; EGF-like.
DR Interpro: IPR002870; Pep_M12b_propep.
DR Interpro: IPR001590; Reprolysin.
DR Interpro: IPR000130; Zn_MTPpeptidse.
DR Pfam; PR00200; disintegrin; 1.
DR Pfam; PF01562; pep_M12b_propep; 1.
DR Pfam; PF01421; Reprolysin; 1.
DR ProDom; PD000664; Disintegrin; 1.
DR SMART; SM00050; DISIN; 1.
DR SMART; SM00181; EGF; 1.
DR PROSITE; PS50215; ADAM_MERPRO; 1.
DR PROSITE; PS50214; DISINTEGRIN_2; 1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW Signal; Glycoprotein; Transmembrane; EGF-like domain; zinc;
KW Metal-binding; 1
FT CHAIN 30 845
FT DOMAIN 30 698
FT TRANSMEM 699 718
FT DOMAIN 719 845
FT DOMAIN 413 503
FT DOMAIN 505 634
FT DOMAIN 644 698
FT METAL 347 347
FT ACT_SITE 348 348
FT METAL 351 351
FT METAL 357 357
FT CARBOHYD 144 144
FT CARBOHYD 154 154
FT CARBOHYD 231 231
FT CARBOHYD 381 381
FT CARBOHYD 487 487
FT CARBOHYD 636 636
SQ SEQUENCE 845 AA: 92049 MW: 1756289DA61674 CRC64;

Query Match 9.6%; Score 392.5; DB 11; Length 845;
Best Local Similarity 25.3%; Pred. No. 1.6e-23;
Matches 162; Conservative 94; Mismatches 254; Indels 131; Gaps 33;

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QY 9 LILSM--AAGMG---QYGNPLKRYIRHYGLSYNVDLSHQKQRAKRAVSHEDQFLRID 63
DB 12 LRLRWLLACGLIPVLEAGRPDLQYVHLS--SYETITPRLTRERREALGPPSSQDISYV 69
QY 64 FHHGRHFNRMKRDYSLFDEFKVENSNK---VLDYD--SHI-YTGHYVEEESLA- 115
DB 70 IQAGKGRHITHLRNDLPLNDYVVTYDKESGLSDHPVOSHCHRYGVESGVNSAVA 129
QY 116 -----MGLLMEDLKSSRLVVAHMFEPARYIKRRTLPHSVYIHEDDINPHKYG 168

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Db 130 VSACFGRLGLHLEN-----ASFGIEPLH-----NSSHEHIFYPMDGI---HQEP 172
QY 169 POGGCAHDHSHFEMMKRYQMTGVEEVTOIQOEHAANGPELKKRTNSAEKNTCOLYIOT 228
Db 173 LRCGVSNRDT-----EKEGTQGDDEEH-PSVTQLRRRRRAVLPOTRYVELLIV 220
QY 229 DHEFFRYYGTR-AYIAOTSSHVAIDTYQTFDFSGIRNISPMVKRIRINTTADKDPY 287
Db 221 DKERYDMGNQYAVREEMRLANYLDSMT-----MLNIRIYLVGLEIWT---DRNPI 271
QY 288 NPERFPNIGVEKPLE-----LNSEQNHDDYCLAYFTDRDDEGVLGLAMVGAAPSGLSSGG 342
Db 272 NIIGAGADVLGNFVQWREKFLITRRRHS---AQLVKKGF-CGTAGMAFVGT----- 320
QY 343 ICEKSKLYSDGKKSLNT-GITVQNYGSHVPPKVSHTIFAHVEGHNFGSPHDSCTECP 401
Db 321 VCSRS--HAGG---INVEQITVETFAIY-----AHELGHNLGMNHDDGRECF 365
QY 402 GESKNLGOKENGNYIYARATSGDKLNNNFSLSIRNISQVLEKKRNOCVE----- 454
Db 366 GAK-----SCIMNSGAS-----GSRNFSCSADPEKLTLANGGSCILNIPKDEA 411
QY 455 SGOPICGNNGVEQEGECDCGYSDCK-DECCFDANOPEGRKCKLKPGKQCSFSGPCCTA 513
Db 412 YSAPSCGNKLVDPGEECDCTAKECEVDPC-----EGSTCKLKSFAEC--AYGDC-K 462
QY 514 QCAFKSKSEKCR-DDSDCAREGICNGFTALCPASDPRPNTDCNRHTOYCINQCAAGSTC 572
Db 463 DCOFLPGGSMCRGKTSCEQVPEYCNSSQPCPPDVFTQNGYPCQNSKAYCYNG-----MC 517
QY 573 EKYGLEECTCASSDGRDKDELCHVCCMKMDP-STCASTGS 612
Db 518 QYDAQOQVIEGSKAKAAPRDCFTFVNSKGRGRCNGCFSGS 558

```

Search completed: April 1, 2002, 15:12:06  
 Job time: 688 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Comugen Ltd.

OM protein - protein search, using sw model

Run on: April 1, 2002, 15:12:06 ; Search time 98.78 Seconds  
(Without alignments)  
392.409 Million cell updates/sec

Title: US-09-871-388-6

Perfect score: 1484  
Sequence: 1 NSEQNHDDYCLAVFTDRDF.....KPNFTDCNHRFQVINGVSI 265

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: SPTRMBL\_17:\*  
2: sp\_archaea:\*  
3: sp\_bacteria:\*  
4: sp\_fungi:\*  
5: sp\_human:\*  
6: sp\_invertebrate:\*  
7: sp\_mmc:\*  
8: sp\_mammal:\*  
9: sp\_organella:\*  
10: sp\_phase:\*  
11: sp\_plant:\*  
12: sp\_podent:\*  
13: sp\_virus:\*  
14: sp\_vertebrate:\*  
15: sp\_unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1472	99.2	691	4	010742
2	1472	99.2	748	4	014672
3	1466	98.8	544	11	010743
4	1463	98.6	749	11	035598
5	1449	97.6	748	6	010741
6	754	50.8	1537	5	09VA12
7	737	49.7	1236	5	09NKR9
8	737	49.7	1238	5	09VJW9
9	737	49.7	1239	5	094902
10	683	46.0	922	5	046354
11	406	27.4	75	6	077633
12	390	26.3	162	13	042568
13	366	24.7	686	5	094316
14	298.5	20.1	600	13	09PVK7
15	293	19.7	620	13	042138
16	292.5	19.7	610	13	09DGB9
17	291.5	19.6	845	11	061072
18	290	19.5	728	4	09BZ11
19	289.5	19.5	609	13	090282

20	286.5	19.3	819	4	013443	013443 homo sapien
21	282.5	19.0	914	13	012960	012960 xenopus lae
22	282	19.0	610	13	09Y120	09Y120 agkistrodon
23	280.5	18.9	920	11	035674	035674 mus musculu
24	280	18.9	609	13	09W6M5	09W6M5 agkistrodon
25	280	18.9	610	13	093523	093523 bothrops ja
26	279	18.8	606	13	098UP9	098UP9 bothrops ja
27	277.5	18.7	604	13	09PT48	09PT48 atractaspis
28	273	18.4	616	13	090495	090495 echis carin
29	270	18.2	735	11	060411	060411 cavia porce
30	269.5	18.2	637	11	09R158	09R158 mus musculu
31	269.5	18.2	873	13	042595	042595 xenopus lae
32	268	18.1	419	13	092043	092043 croctalus at
33	267.5	18.0	857	4	09UH2	09UH2 homo sapien
34	267.5	18.0	918	4	09H013	09H013 homo sapien
35	267.5	18.0	918	4	09BZ15	09BZ15 homo sapien
36	267	18.0	1369	5	09VPH0	09VPH0 drosophila
37	262	17.7	761	11	09R160	09R160 mus musculu
38	261	17.6	788	11	035227	035227 mus musculu
39	259	17.5	451	13	09PT49	09PT49 atractaspis
40	257	17.3	505	13	073795	073795 agkistrodon
41	257	17.3	617	13	090499	090499 echis pyram
42	257	17.3	789	11	063180	063180 rattus norv
43	254	17.1	903	11	061824	061824 mus musculu
44	253	17.0	685	5	09VXL1	09VXL1 drosophila
45	253	17.0	694	5	09GZ15	09GZ15 drosophila

## ALIGNMENTS

RESULT	ID	1	PRELIMINARY:	PRT:	691 AA.
010742	010742	092650:			
AC	010742	01-NOV-1996 (TREMBLrel. 01, Created)			
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)				
DE	DISINTEGRIN-METALLOPROTEINASE MADM (FRAGMENT).				
OS	Homo sapiens (human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_Taxid:9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=6276398; PubMed=8694785;				
RA	Howard L., Lu X., Mitchell S., Griffiths S., Glynn P.;				
RT	"Molecular cloning of MADM: a catalytically active mammalian				
RT	RT disintegrin-metalloprotease expressed in various cell types."				
RL	Biochem. J. 317:45-50(1996).				
DR	EMBL: Z48579; CA08463.1; .				
DR	HSSP: P18619; 1FVL.				
DR	MEROPS: M12.210; .				
DR	InterPro: IPR001762; Disintegrin.				
DR	InterPro: IPR001590; Repolysin.				
DR	InterPro: IPR001130; Zn_MTPeptide.				
DR	Pfam: PF00200; disintegrin; 1.				
DR	Pfam: PF01421; Repolysin; 1.				
DR	PRINTS: PR00289; DISINTEGRIN.				
DR	SMART: SM00050; DISIN: 1.				
DR	PROSITE: PS50215; ADAM_MEPRO: 1.				
DR	PROSITE: PS50214; DISINTEGRIN_2: 1.				
DR	PROSITE: PS00142; ZINC_PROTEASE; UNKNOWN_1.				
KW	Integrin.				
FT	NON_TER				
FT	NON_TER				
SQ	SEQUENCE	691 AA;	77632 MW;	8B43698F24B6R292	CRC64;

Query Match 99.2%; Score 1472; DB 4; Length 691;  
Best Local Similarity 100.0%; Pred. No. 1.8e-131;  
Matches 262; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 247 NSEQNHDDYCLAYVFTDRDFDGVGLAVGAPSGSSGGICCKSKLYSDGKKSLNTGII 306  
 QY 61 TVQNTGSHVPPKVSHTTFAHVGHNFGSPHDSGTCTPESKNLCKEKGNTIMARATS 120  
 Db 307 TVQNTGSHVPPKVSHTTFAHVGHNFGSPHDSGTCTPESKNLCKEKGNTIMARATS 366  
 QY 121 GDLNNKSFSLCSIRNISQVLEKRRNCFVESGQPICGNGVYEGEBCDCGYSDCKDEC 180  
 Db 367 GDLNNKSFSLCSIRNISQVLEKRRNCFVESGQPICGNGVYEGEBCDCGYSDCKDEC 426  
 QY 181 CFDPANPEGRKCKLPGKQCSPOGCTAOCFAKSKSKCRDDSDCARREGICNGFTALC 240  
 Db 427 CFDPANPEGRKCKLPGKQCSPOGCTAOCFAKSKSKCRDDSDCARREGICNGFTALC 486  
 QY 241 PASDPKPNFTDCNRHTQVING 262  
 Db 487 PASDPKPNFTDCNRHTQVING 508

RESULT 2  
 014672 PRELIMINARY: PRT: 748 AA.  
 AC 014672: 01-JAN-1998 (TREMBLrel. 05, Created)  
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE ADAM10.  
 GN ADAM10.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OX NCBI\_Taxid:9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE:97450992; PubMed:9305925;  
 RA Rosendahl M.S., Ko S.C., Long D.L., Brewer M.T., Rosenzweig B.,  
 RA Hedi E., Anderson L., Pyle S.M., Moreland J., Meyers M.A., Kohno T.,  
 RA Lyons D., Lichenstein H.S.;  
 RT Identification and characterization of a pro-tumor necrosis factor-  
 RT alpha-processing enzyme from the ADAM family of zinc  
 RT metalloproteases.\*;  
 RT J. Biol. Chem. 272:24588-24593(1997).  
 RU EMBL: AF009615; AAC51766.1; --  
 DR HSSP: P18619; 1FVL.  
 DR InterPro: IPR001762; Disintegrin.  
 DR InterPro: IPR001590; Reprolysin.  
 DR InterPro: IPR00130; Zn\_MTPeptidse.  
 DR Pfam: PF00200; disintegrin; 1.  
 DR Pfam: PF01421; Reprolysin; 1.  
 DR SMART: SM00050; DISIN; 1.  
 DR PROSITE: PS50215; ADAM\_MEPRO; 1.  
 DR PROSITE: PS50214; DISINTEGRIN\_2; 1.  
 DR PROSITE: PS00142; ZINC\_PROTEASE; UNKNOWN\_1.  
 DR PROSITE: PS00142; ZINC\_PROTEASE; UNKNOWN\_1.  
 SQ SEQUENCE 748 AA; 84142 MW; 088165B17022A71 CRC64;

Query Match 99.2%; Score 1472; DB 4; Length 748;  
 Best Local Similarity 100.0%; Pred. No. 2e-131;  
 Matches 262; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 NSEQNHDDYCLAYVFTDRDFDGVGLAVGAPSGSSGGICCKSKLYSDGKKSLNTGII 60  
 Db 304 NSEQNHDDYCLAYVFTDRDFDGVGLAVGAPSGSSGGICCKSKLYSDGKKSLNTGII 363  
 QY 61 TVQNTGSHVPPKVSHTTFAHVGHNFGSPHDSGTCTPESKNLCKEKGNTIMARATS 120  
 Db 364 TVQNTGSHVPPKVSHTTFAHVGHNFGSPHDSGTCTPESKNLCKEKGNTIMARATS 423  
 QY 121 GDLNNKSFSLCSIRNISQVLEKRRNCFVESGQPICGNGVYEGEBCDCGYSDCKDEC 180  
 Db 424 GDLNNKSFSLCSIRNISQVLEKRRNCFVESGQPICGNGVYEGEBCDCGYSDCKDEC 483

QY 181 CFDPANPEGRKCKLPGKQCSPOGCTAOCFAKSKSKCRDDSDCARREGICNGFTALC 240  
 Db 484 CFDPANPEGRKCKLPGKQCSPOGCTAOCFAKSKSKCRDDSDCARREGICNGFTALC 543  
 QY 241 PASDPKPNFTDCNRHTQVING 262  
 Db 544 PASDPKPNFTDCNRHTQVING 565

RESULT 3  
 010743 PRELIMINARY: PRT: 544 AA.  
 AC 010743: 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE DISINTEGRIN-METALLOPROTEASE PRECURSOR (EC 3.4.24.-) (MYELIN-ASSOCIATED  
 DE METALLOPROTEINASE) (MADM) (FRAGMENT).  
 DE Rattus norvegicus (Rat).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_Taxid:10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;  
 RX MEDLINE:96276398; PubMed:8694785;  
 RA Howard L., Mitchell S., Lu X., Griffiths S., Glynn P.;  
 RT Molecular cloning of MADM: a catalytically active mammalian  
 RT disintegrin-metalloprotease expressed in various cell types.\*;  
 RL Biochem. J. 317:45-50(1996).  
 CC -1 SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
 CC -1 SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B (ZINC  
 CC METALLOPROTEASE); ALSO KNOWN AS THE REPROLYSIN SUBFAMILY.  
 CC -1 SIMILARITY: HIGH, IN THE MIDDLE REGION, TO DISINTEGRIN.  
 DR EMBL: Z48444; CAA88359.1; --  
 DR HSSP: P18619; 1FVL.  
 DR MEROPS: M12.210; --  
 DR InterPro: IPR001762; Disintegrin.  
 DR InterPro: IPR001590; Reprolysin.  
 DR InterPro: IPR00130; Zn\_MTPeptidse.  
 DR Pfam: PF00200; disintegrin; 1.  
 DR Pfam: PF01421; Reprolysin; 1.  
 DR PRINTS: PR00289; DISINTEGRIN.  
 DR SMART: SM00050; DISIN; 1.  
 DR PROSITE: PS50215; ADAM\_MEPRO; 1.  
 DR PROSITE: PS50214; DISINTEGRIN\_2; 1.  
 DR PROSITE: PS00142; ZINC\_PROTEASE; UNKNOWN\_1.  
 KW Integrin; Hydrolyase; Metalloprotease; Transmembrane; Zinc; Signal;  
 KW Glycoprotein.  
 FT NON\_TER 1 1  
 FT SIGNAL <1 9  
 FT CHAIN 10 241 METALLOPROTEINASE.  
 FT CHAIN 242 346 DISINTEGRIN.  
 FT DOMAIN 10 468 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 469 492 POTENTIAL.  
 FT DOMAIN 493 544 CYTOPLASMIC (POTENTIAL).  
 FT ACT\_SITE 180 180 BY SIMILARITY.  
 FT METAL 179 179 ZINC (CATALYTIC) (BY SIMILARITY).  
 FT METAL 183 183 ZINC (CATALYTIC) (BY SIMILARITY).  
 FT METAL 189 189 ZINC (CATALYTIC) (BY SIMILARITY).  
 FT CARBOHYD 63 63 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 74 74 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 235 235 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 347 347 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 544 AA; 60444 MW; F75B0EB06C88A7DD CRC64;

Query Match 98.8%; Score 1466; DB 11; Length 544;  
 Best Local Similarity 99.2%; Pred. No. 5.1e-131;  
 Matches 260; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 NSEQNHDDYCLAYVFTDRDFDGVGLAVGAPSGSSGGICCKSKLYSDGKKSLNTGII 60  
 Db 304 NSEQNHDDYCLAYVFTDRDFDGVGLAVGAPSGSSGGICCKSKLYSDGKKSLNTGII 363

D6	100	NSEONHDDYCLAYFTETDRDFDGYGLAWGAPSGSSGGJCEKSKLTSDKKKSLNFI	159
QY	61	TVOVNGSHVPKVBHITFAHEVGNFNSPHDSGECPGESKNLNGOKENNYIMATATS	120
D6	160	TVOVNGSHVPKVBHITFAHEVGNFNSPHDSGETCPGESKNLNGOKENNYIMATATS	219
QY	121	GDKLNNNKFSLSIRNTISOYLEKRRNNCFVESGPICGNMGVEOEGECDCGYSDQCDEC	180
D6	220	GDKLNNNKFSLSIRNTISOYLEKRRNNCFVESGPICGNMGVEOEGECDCGYSDQCDEC	279
QY	181	CFDANOPBGRCKLKPGKQCSPSOGPCCTAQCAFKSKSEKCRDSDCAREGICNGFTALC	240
D6	280	CFDANOPBGRCKLKPGKQCSPSOGPCCTAQCAFKSKSEKCRDSDCAREGICNGFTALC	339
QY	241	PASDPKPFMTDNHRHTOVCIING	262
D6	340	PASDPKPFMTDNHRHTOVCIING	361

RESULT	4	
ID	035598	PRELIMINARY; PRT; 749 AA.
AC	035598;	
DT	01-JAN-1998 (TREMBLrel. 05, Created)	
DT	01-JAN-1998 (TREMBLrel. 05, Last sequence update)	
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)	
DE	KUZBAIAN.	
GN	ADAM10 OR MKUZ.	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.	
OX	NCBI_Taxid=10090;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
FX	MEDLINE=97386452; PubMed=9244301;	
RA	Pan D., Rubin G.M.;	
RT	"Kuzbanian controls proteolytic processing of Notch and mediates	
RT	lateral inhibition during Drosophila and vertebrate neurogenesis."	
RL	Cell 90:271-280(1997).	
DR	EMBL; AF011379; AAC53303.1; -.	
DR	HSSP; PI8619; IEVL.	
DR	MEROPS; M12.211; -.	
DR	MGD; MGI:109548; Adam10.	
DR	InterPro: IPR001762; Disintegrin.	
DR	InterPro: IPR001590; Repolysin.	
DR	InterPro: IPR000130; Zn_MTPeptide.	
DR	Pfam: PF00200; disintegrin; 1.	
DR	Pfam: PF01421; Repolysin; 1.	
DR	SMART; SM00050; DISIN; 1.	
DR	PROSITE; PSS0215; ADAM_MPRO; 1.	
DR	PROSITE; PSS0214; DISINTEGRIN_2; 1.	
DR	PROSITE; PSS0142; ZINC_PROTEASE; UNKNOWN.1.	
SO	SEQUENCE 749 AA: 83966 MW: 06C6C3EB2C5FF94 CRC64;	

Query Match:	98.6%	Score 1463:	DB 11:	Length 749:
Best Local Similarity	98.9%	Pred. No. 1,4e-110:		
Matches 259:	Conservative	3:	Mismatches 0:	Indels 0:
Gaps				0
QY	1	NSEDNHDDYCLAYVFDPRDFDGVGLANVCAPSSSSGICEKSKLYSOGKKSLNTGII	60	
Db	305	NSEDNHDDYCLAYVFDPRDFDGVGLANVCAPSSSSGICEKSKLYSOGKKSLNTGII	364	
QY	61	TVNYGSHVPKSHSTTFAHEVGHNGFSPHDSGTCTGEGESKNLGOKENYIMYARATS	120	
Db	365	TVNYGSHVPKSHSTTFAHEVGHNGFSPHDSGTCTGEGESKNLGOKENYIMYARATS	424	
QY	121	GDKLNNNKFSLCISIRNISOVLEKKRNKNCVEGQETICNGMVEGGEBCDCYSPOQKDEC	180	
Db	425	GDKLNNNKFSLCISIRNISOVLEKKRNKNCVEGQETICNGMVEGGEBCDCYSPOQKDEC	484	
QY	181	CFDANPQEGKKCLKTRGKQCSFSGPCCCTACGAFKSKSEKCRDSDCARBETICNGFTALC	240	

<b>Dd</b>	<b>485</b>	CFDANQEPGKKCKLKPGKQCSPSGPCTQAACAKSKSEKCRDPSDACKEIGICNGFTALC	<b>544</b>
<b>Dy</b>	<b>241</b>	PASDPKRPFITDCNRHRYCYCING	<b>262</b>
<b>Dd</b>	<b>545</b>	PASDPKRPFITDCNRHRYCYCING	<b>566</b>

RESULT	5	
ID	010741	PRELIMINARY; PRT; 748 AA.
AC	010741;	
DT	01-NOV-1996 (TREMBLrel. 01, Created)	
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)	
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)	
DE	DISINTEGRIN-METALLOPROTEINASE PRECURSOR (EC 3.4.24.-) (MYELIN-ASSOCIATED METALLOPROTEINASE) (MADPM).	
OS	Bos taurus (Bovine).	
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;	
OC	Bovidae; Bovinae; Bos.	
OX	NCBI_TaxID=9913;	
RN	[1]	
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.	
RC	TISSUE=BRAIN;	
RX	MEDLINE=96276398; PubMed=8694785;	
RA	Howard L., Lu X., Mitchell S., Griffiths S., Glynn P.;	
RT	"Molecular cloning of MADPM: a catalytically active mammalian disintegrin-metalloprotease expressed in various cell types.";	
RL	Biochem. J. 317:45-50(1996).	
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.	
CC	-1- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN BRAIN. AT LOWER LEVELS IN KIDNEY, SPLEEN, LUNG AND HEART.	
CC	-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M2C (ZINC METALLOPROTEASE).	
CC	-1- SIMILARITY: HIGH, IN THE MIDDLE REGION, TO DISINTEGRINS.	
DR	EMBL; Z21961; CAA79973.1; -.	
DR	HSSP; P18619; 1FVL.	
DR	MEROPS; M12.210; -.	
DR	InterPro; IPR001762; Disintegrin.	
DR	InterPro; IPR001590; Repolysin.	
DR	InterPro; IPR000130; Zn_MTPase.	
DR	Pfam; PF00200; disintegrin; 1.	
DR	Pfam; PF01421; Repolysin; 1.	
DR	SMART; SM00050; DISIN; 1.	
DR	PROSITE; PS50215; ADAM_MEROP; 1.	
DR	PROSITE; PS50214; DISINTEGRIN_2; 1.	
DR	PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.	
KW	Integrin; Hydrolase; Metalloprotease; Transmembrane; Zinc; Signal; Glycoprotein.	
KW	Signal.	
FT	SIGNAL	1
FT	PROPEP	20
FT	CHAIN	214
FT	CHAIN	456
FT	CHAIN	550
FT	DOMAIN	20
FT	DOMAIN	673
FT	TRANSMEM	697
FT	DOMAIN	748
FT	ACT_SITE	384
FT	METAL	383
FT	METAL	387
FT	METAL	387
FT	METAL	393
FT	CARBOHYD	267
FT	CARBOHYD	278
FT	CARBOHYD	439
FT	CARBOHYD	551
SO	SEQUENCE	748 AA; 8418 MW; 202829630611F9E1 CRC64;

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Query Match      97.68;  Score 1449;  DB 6;  Length 740;
Best Local Similarity 97.78;  Pred. No. 3e-129;
Matches 256;  Conservative 4;  Mismatches 2;  Indels 0;  Gaps 0.

QY      1 NSRQHHDYCLAVFPPDRDFDDGVLGLMVGAPSSSSGGICEKSLKSDKKKSLINGI 60
|||||

```

DB 304 NSQNHDDYCLAVFTDRDFDDGVLGLAWGAPSGSSGGICEKSKLYSDGKKSLNTGII 363  
 QY 61 TVONYSHPVKYSHITPAHEVGNFGSPHDSGECTPGESKNLGGKENGNTIMARATS 120  
 DB 364 TVONYSHPVKYSHITPAHEVGNFGSPHDSGECTPGESKNLGGKENGNTIMARATS 423  
 QY 121 GDLNNKFSLSISIRISQVLEKRRNCFVESGQPICGNGMVBQEGECGYSDDCKDEC 180  
 DB 424 GDLNNKFSLSISIRISQVLEKRRNCFVESGQPICGNGMVBQEGECGYSDDCKDEC 483  
 QY 181 CFANQPEGKKCKLKPGKQCSQSGPCCCTAQCFAFKSKSEKCRDSDCAREGICNGTALC 240  
 DB 484 CYANQPEGKKCKLKPGKQCSQSGPCCCTAQCFAFKSKSEKCRDSDCAREGICNGTALC 543  
 QY 241 PASDPKPNFTDGNRHTQVING 262  
 DB 544 PASDPKPNFTDGNRHTQVING 565

RESULT 6  
 ID Q9VA12 PRELIMINARY: PRT: 1537 AA.  
 AC Q9VA12:  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE CG1964 PROTEIN.  
 GN CG1964.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 ON NCBI\_TaxID=7227;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BERKELEY;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.H.C., Blazey R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Milos G.L.G.,  
 RA Abril J.F., Adganyi A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borkov D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,  
 RA Burlis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodok A., Gong F., Gorell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalali M., Kalish F., Kapen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Mishina N.V., Modyaty C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard C., Scheeler F., Shen T.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheller P., Smith H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spletzer E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RT "The genome sequence of Drosophila melanogaster."  
 RL Science 287:2185-2195(2000).  
 CC -I- SIMILARITY: TO NEUTRAL ZINC METALLOPEPTIDASES, ZINC-BINDING REGION  
 CC DOMAIN.  
 DR EMBL: AE003770; AAF56926.1; -.  
 DR HSSP: P18619; IYVL.  
 DR FlyBase: FBgn0039688; CG1964.  
 DR InterPro: IPR001762; Disintegrin.  
 DR InterPro: IPR001590; Reprolysin.  
 DR InterPro: IPR000130; Zn\_MTPeptidse.  
 DR Pfam: PF01421; Reprolysin; 1.  
 DR SMART: SM00050; Disin; 1.  
 DR PROSITE: PS50215; ADAM\_MEPRO; 2.  
 DR PROSITE: PS50214; DISINTEGRIN; 2; 1.  
 DR PROSITE: PS00142; ZINC\_PROTEASE; 1.  
 DR Hydrolase; Metalloprotease; Zinc.  
 KW SEQUENCE 1537 AA; 168796 MW; 46A52344A8E73617 CRC64;

Query Match 50.8%; Score 754; DB 5; Length 1537;  
 Best Local Similarity 54.3%; Pred. No. 6,26-63;  
 Matches 145; Conservative 33; Mismatches 71; Indels 18; Gaps 9;

QY 2 SEQNHDDYCLAVFTDRDFDDGVLGLAWGAPSGSSGGICEKSKLYSDGKKSLNTGII 61  
 DB 566 SEEDYDAFLAVFTYRDFEMGTGLAWTG-DLNAGVCEKNCHYR-GSLKSLNTGIVT 623  
 QY 62 YONYSHPVKYSHITPAHEVGNFGSPHDSGECTPGESKNLGGKENGNTIMARATS 121  
 DB 624 LNTYKHHPPAVSHYTLAHEIGHNFGSPHD-EQCTPG-----GEGNNTIMARATS 675  
 QY 122 GDLNNKFSLSISIRISQVLEKRRNCFVESGQPICGNGMVBQEGECGYSDDCKD 178  
 DB 676 GDLNNKFSLSISIRISQVLEKRRNCFVESGQPICGNGMVBQEGECGYSDDCKD 735  
 QY 179 ECCFPD-ANPD-EGKKCKLKPGKQCSQSGPCCCTAQCFAFKSKSEKCRDSDCAREGICNG 235  
 DB 736 SCCFPMSRPRDEHPCTLTPHARCSPSQGPCTTDCKLKF-GDKCRDSDCAREGICNG 794  
 QY 236 FALCPASDPKPNFTDGNRHTQVING 262  
 DB 795 RVPQCPSPVKNPKTKITCNKEF-VCTMG 820

RESULT 7  
 ID Q9NKF9 PRELIMINARY: PRT: 1236 AA.  
 AC Q9NKF9:  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE KUZ PROTEIN.  
 GN KUZ OR BG:DS07660.3 OR CG7147.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 ON NCBI\_TaxID=7227;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-Y, CN BW SP;  
 RX MEDLINE=99403001; PubMed=10471707;  
 RA Ashburner M., Misra S., Roote J., Lewis S.E., Blazey R., Davis T.,  
 RA Doyle C., Galle R., George R., Harris N., Hartzell G., Harvey D.,  
 RA Hong L., Houston K., Hoskins R., Johnson G., Martin G., Moshrefi A.,  
 RA Palazzolo M., Reese M.G., Spradling A., Tsang G., Wan K., Whitelaw K.,  
 RA Celniker S., Rubin G.M.;  
 RT "An exploration of the sequence of a 2.9-Mb region of the genome of  
 RT Drosophila melanogaster: the Adh region.";  
 RL Genetics 153:179-219(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-Y, CN BW SP;







Query Match 27.4%; Score 406; DB 6; Length 75;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-31;  
 Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY PHDSGTECPGSKNLGKENGNYIMYARATSGDILNNKPSLCSIRINSQYLEKRRNC 148  
 DB 1 PHDSGTECPGSKNLGKENGNYIMYARATSGDILNNKPSLCSIRINSQYLEKRRNC 60

OY 149 FVSGGPICGNGME 163  
 DB 61 FVSGGPICGNGME 75

RESULT 12  
 O42568 PRELIMINARY; PRT; 162 AA.

ID O42568  
 AC O42568;  
 DT 01-JAN-1998 (TREMBLrel. 05, Created)  
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE KUZBANIAN (FRAGMENT).  
 GN XK02.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Mesodactyla; Pipidea; Pipidae;  
 OC Xenopodinae; Xenopus.  
 NX NCBI\_TaxID=8355;  
 RX MEDLINE=97386452; PubMed=9244301;  
 RA Pan D., Rubin G.M.;  
 RT "Kuzbanian controls proteolytic processing of Notch and mediates  
 RT lateral inhibition during Drosophila and vertebrate neurogenesis.";  
 RL Cell 90:271-280(1997).  
 DR EMBL: AF011380; AAC60248.1; .  
 DR HSSP: P16619; 1FVL.  
 DR MEROPS: M12.210; .  
 DR InterPro: IPR001762; Disintegrin.  
 DR PRINTS: PR00289; DISINTEGRIN.  
 DR SMART: SM00050; DISIN. 1.  
 DR PROSITE: PS50214; DISINTEGRIN\_2; 1.  
 FT NON\_TER 1  
 FT NON\_TER 162  
 FT SEQUENCE 162 AA; 17780 MW; E2E0BE1670494492 CRC64;

Query Match 26.3%; Score 390; DB 13; Length 162;  
 Best Local Similarity 70.3%; Pred. No. 1.8e-29;  
 Matches 64; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

OY 172 YSDCKDECCFDANQPEGRKCKLRKQCSPOGCTAOCAPKSKSEKCHDSDCARREG 231  
 DB 1 YSDCKDECCFDANQPEGRKCKLRKQCSPOGCTAOCAPKSKSEKCHDSDCARREG 60

OY 232 ICNGFTALCPASDPKPNFTDCNRHTQVCING 262  
 DB 61 TCNGNSACPPSEPRENLTECNRAIOVCING 91

RESULT 13  
 O94316 PRELIMINARY; PRT; 666 AA.

ID O94316  
 AC O94316;  
 DT 01-FEB-1997 (TREMBLrel. 02, Created)  
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE SIMILARITY TO METALLOPROTEASES.  
 GN ZK154.7.  
 OS Caenorhabditis elegans.  
 CC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 CC Rhabditidae; Peleoderinae; Caenorhabditis.  
 NX NCBI\_TaxID=6239;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL N2;  
 RX MEDLINE=94150718; PubMed=7906398;  
 RA Wilson R., Ainsworth R., Anderson K., Baynes C., Berks M.,  
 RA Bonfield J., Burton J., Connell M., Copey T., Cooper J., Coulson A.,  
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,  
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,  
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,  
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,  
 RA Parsons J., Percy C., Riken L., Koopa A., Saunders D., Showkeen R.,  
 RA Smalton N., Smith A., Sonhammer E., Staden R., Sulston J.,  
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterson R.,  
 RA Watson A., Weinstock L., Wilkinson-Spratt J., Woldman P.;  
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
 RT elegans.";  
 RL Nature 368:32-38(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL N2;  
 RA Connell M.;  
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL N2;  
 RA Waterson R.;  
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: U70844; AAB09097.1; .  
 DR HSSP: P17494; 1KST.  
 DR InterPro: IPR001762; Disintegrin.  
 DR InterPro: IPR001590; Repolysin.  
 DR InterPro: IPR001330; Zn\_MTpeptidase.  
 DR SMART: SM00050; DISIN. 1.  
 DR PROSITE: PS50215; ADAM\_MERPRO. 1.  
 DR PROSITE: PS50214; DISINTEGRIN\_2; 1.  
 DR PROSITE: PS00142; ZINC\_PROTEASE; UNKNOWN. 1.  
 KW Protease; Metalloprotease.  
 SQ SEQUENCE 686 AA; 77298 MW; 66D58008A207AE49 CRC64;

Query Match 24.7%; Score 366; DB 5; Length 686;  
 Best Local Similarity 33.1%; Pred. No. 1.7e-26;  
 Matches 91; Conservative 40; Mismatches 112; Indels 32; Gaps 10;

OY 8 DYCIVAYFTDPDPPD-GVLGLAWGAP--SGSSGTCESKSLSDGKKSLNTGITT--V 62  
 DB 292 DFCIVHLYTARTREAVTLGLAVSYKKWDPTAGTCKOET--NGRVAYINVLSTSF 350

OY 63 QNKGSHVP--PKVSHITFAHEVGHNEGSPHD-----SGFECTPGESKSLGOKENGNY 112  
 DB 351 NSEOSTYPLITKEIDIVSHYEGHAMGATHDPTIDSDDPVEECSPND-----QNGCKY 404

OY 113 IMYARATSGKLNKPSLCSIRINSQYLEKRRNCNVEGQPICGNGVGECEDCG 172  
 DB 405 LMSQYAKGQYDANNVLESPCSRLIRVLLIGKWSQFQEBMTSFCNGIVGECEDCN 464

OY 173 SDOCKDECCFDANQPEGRKCKLRKQCSPOGCTAOCAPKSKSEKCHDSDCARREG 230  
 DB 465 DTONEFNC-----DKRCILAVGAKCSPLNIHICTPTGCFHNSHVCILPDSLCKAD 517

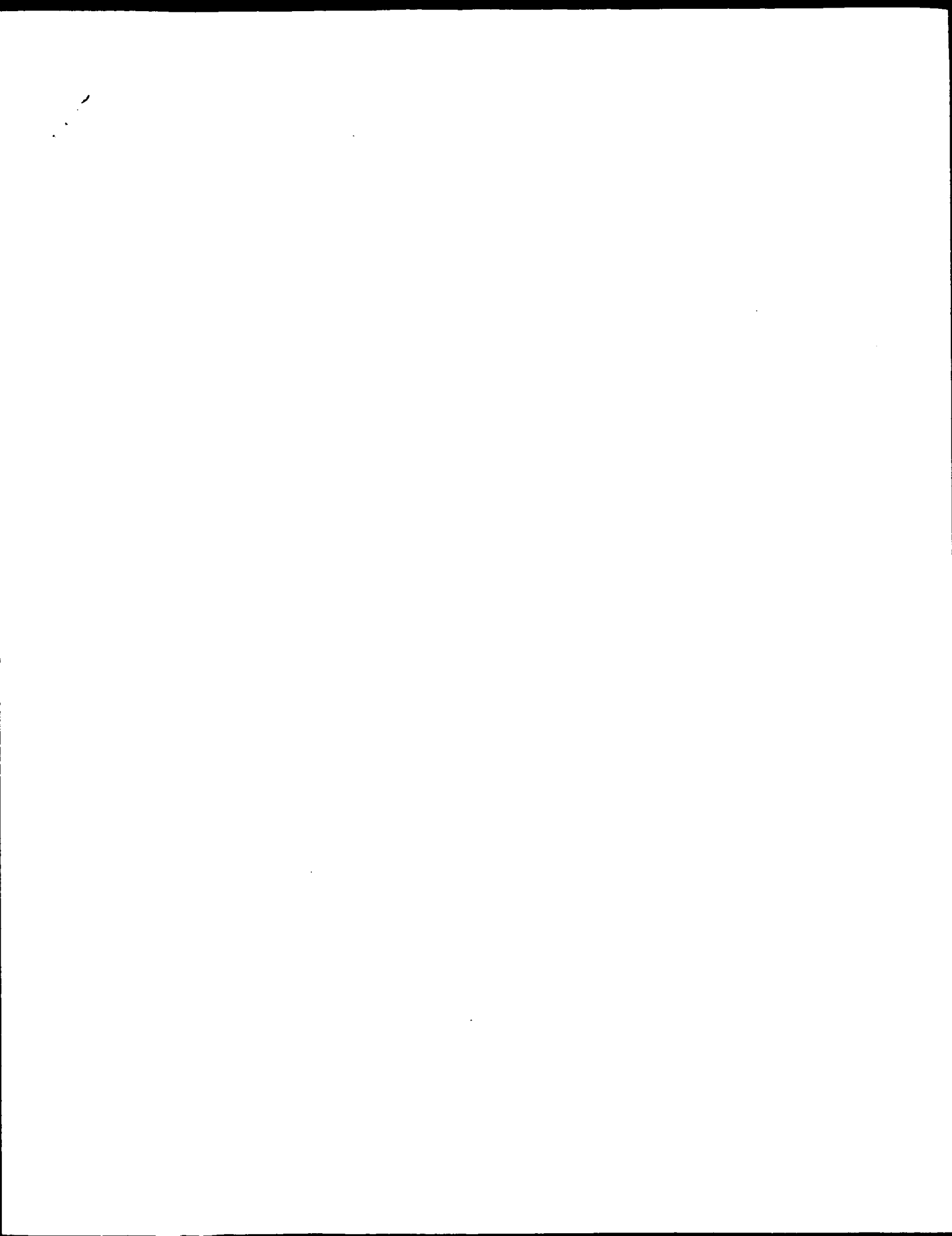
OY 231 GICNGFTALCPASDPKPNFTDCNRHTQVCING 265  
 DB 518 AVCNGFSGECPAPVPVGDQGECLGEG-CLNGVCL 551

RESULT 14  
 O9PVK7 PRELIMINARY; PRT; 600 AA.

ID O9PVK7  
 AC O9PVK7;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE COBRIN PRECURSOR.







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OM protein - protein search, using sw model

Run on: April 1, 2002, 15:12:07 ; Search time 98.78 Seconds

(without alignments)  
1109.111 Million cell updates/sec

Title: US-09-871-388-8

Perfect score: 4103  
Sequence: 1 MYLPTVLLILLISWAGLGGO.....100PPRORPRESYGMHMR 749

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_17:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4103	100.0	749	11	035598 mus musculu
2	3940.5	96.0	748	4	014672 homo sapien
3	3884.5	94.7	748	6	010741 bos taurus
4	3346	81.6	691	4	010742
5	2956	72.0	544	11	010743
6	1489.5	36.3	1238	5	09VW9
7	1489	36.3	1239	5	094902
8	1487.5	36.3	1236	5	09NKF9
9	1397	34.0	922	5	046354
10	1352	33.0	1537	5	09VA12
11	707	17.2	162	13	042568
12	478	11.7	686	5	094316
13	416.5	10.2	845	11	061072
14	409	10.0	600	13	09PVK7
15	406	9.9	75	6	077633
16	395.5	9.6	819	4	013443
17	385	9.4	616	13	090495
18	384.5	9.4	604	13	09PT48
19	380.5	9.3	873	13	042595

20	377.5	9.2	610	13	09DGB9
21	375	9.1	914	13	012960
22	372	9.1	620	13	042138
23	365	8.9	735	11	060411
24	361.5	8.8	920	11	035674
25	360	8.8	617	13	090499
26	351.5	8.6	728	4	09B211
27	350	8.5	609	13	090282
28	348	8.5	505	13	073795
29	345.5	8.4	606	13	098UP9
30	345.5	8.4	610	13	09Y120
31	343.5	8.4	609	13	09W6M5
32	337.5	8.2	1569	5	09VFEH0
33	337	8.2	760	11	09D4E4
34	337	8.2	918	4	09H013
35	337	8.2	918	4	09B215
36	333.5	8.1	610	13	093523
37	333	8.1	760	11	09R159
38	332.5	8.1	832	4	075077
39	329.5	8.0	829	11	09R1V7
40	328	8.0	697	11	09R158
41	326	7.9	419	13	092043
42	324.5	7.9	549	13	090500
43	324.5	7.9	857	4	090HP2
44	323.5	7.9	903	11	061824
45	323	7.9	739	4	09Y307

#### ALIGNMENTS

```
RESULT 1
035598 PRELIMINARY: PRT: 749 AA.
AC 035598;
DT 01-JAN-1998 (TREMblrel. 05, Created)
DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE KUZBANIAN.
GN ADAM10 OR MKU2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97386452; PubMed=9244301;
RA Pan D., Rubin G.M.;
RT "Kuzbanian controls proteolytic processing of Notch and mediates
RT lateral inhibition during Drosophila and vertebrate neurogenesis.";
RL Cell 90:271-280(1997).
DR EMBL: AF011379; AAC53303.1; -.
DR HSSP: P18619; LEVL.
DR MEROPS: M12.211; -.
DR MGD: MGI:109548; Adam10.
DR InterPro: IPR001762; Disintegrin.
DR InterPro: IPR001590; Reprolysin.
DR InterPro: IPR000130; Zn_MTPeptide.
DR Pfam: PF00200; disintegrin; 1.
DR Pfam: PF01421; Reprolysin; 1.
DR SMART: SM00050; DISIN; 1.
DR PROSITE: PS50215; ADAM_MERPRO; 1.
DR PROSITE: PS50214; DISINTEGRIN_2; 1.
DR PROSITE: PS00142; ZINC_PROTEASE; UNKNOWN.1.
SQ SEQUENCE 749 AA; 8396 MW; 06CEC3B2C5FAF94 CRC64;
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Query Match 100.0% Score 4103; DB 11; Length 749;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 749; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 MYLPTVLLILLISWAGLGGOYGNPLNKYIRHYEGLSYNDLSLHOKHORAKRAVSHEDQL 60  
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Db 1 MVLPTVLLLSMAAGLGQGYGNPLNKYIRHYEGLSYVDSLHQKQRAKAVSHEDFL 60
QY 61 LLDFAHGRQPNLRMKRDTSLFSDFEKVEYSNKVLDYDTSHTYTGHIYGEESFSHGSVI 120
Db 61 LLDFAHGRQPNLRMKRDTSLFSDFEKVEYSNKVLDYDTSHTYTGHIYGEESFSHGSVI 120
QY 121 DGRFEGFIKTRGGTYIEPAERYIKDRLPHSHVYIHEDDINYPHKYPOGGCADHSVFE 180
Db 121 DGRFEGFIKTRGGTYIEPAERYIKDRLPHSHVYIHEDDINYPHKYPOGGCADHSVFE 180
QY 181 RMRKQMTGVEEGARAHBEKHAASGPELRRKRTTLAERNTCOLYIOTDHLFFKYGTR 240
Db 181 RMRKQMTGVEEGARAHBEKHAASGPELRRKRTTLAERNTCOLYIOTDHLFFKYGTR 240
QY 241 EAVIAQISSHYKALDTIYQTTDFSGIRNISFVKKRIRINTSDEKPTNPFPPNIGVEK 300
Db 241 EAVIAQISSHYKALDTIYQTTDFSGIRNISFVKKRIRINTSDEKPTNPFPPNIGVEK 300
QY 301 FLELNSEONHDDYCLAYVFTDRDGDVGLAWGAPSGSGGICEKSKLYSDGKKKSLN 360
Db 301 FLELNSEONHDDYCLAYVFTDRDGDVGLAWGAPSGSGGICEKSKLYSDGKKKSLN 360
QY 361 TGIITVQNGSHVPPKVSHTTFAHEVGNFSGPHDSGTECTPGEKSKNLGOKENGNTIWA 420
Db 361 TGIITVQNGSHVPPKVSHTTFAHEVGNFSGPHDSGTECTPGEKSKNLGOKENGNTIWA 420
QY 421 RATSQDKLNNNKFSLSIRINSQVLEKKRNCCFVESGPIGNGMVEQEGECDCGYSQD 480
Db 421 RATSQDKLNNNKFSLSIRINSQVLEKKRNCCFVESGPIGNGMVEQEGECDCGYSQD 480
QY 481 KDCCFPDANOPBGRKCKLPGKQCSPOGCTAOCFAKSKSEKCRDSDCAKEGICNGF 540
Db 481 KDCCFPDANOPBGRKCKLPGKQCSPOGCTAOCFAKSKSEKCRDSDCAKEGICNGF 540
QY 541 TALCPASDPKPRFTDCNRHTOVCLNGQAGSICEKYDLEBCTCASSDKDKNELCYVCCM 600
Db 541 TALCPASDPKPRFTDCNRHTOVCLNGQAGSICEKYDLEBCTCASSDKDKNELCYVCCM 600
QY 601 KMAPSTCAGTSGLOWSKQFSGRITTLQPGSPCNDPFGYCDVFMRCRLVDADGPLARLKK 660
Db 601 KMAPSTCAGTSGLOWSKQFSGRITTLQPGSPCNDPFGYCDVFMRCRLVDADGPLARLKK 660
QY 661 AIFSQLYENTIAEWIVAHMAVLLMGLALMLMAGFIKICSVHTPPSSNPKLPPPKPLPGT 720
Db 661 AIFSQLYENTIAEWIVAHMAVLLMGLALMLMAGFIKICSVHTPPSSNPKLPPPKPLPGT 720
QY 721 LKRRRPPQIPQORQRPRESYQMGHMR 749
Db 721 LKRRRPPQIPQORQRPRESYQMGHMR 749

RESULT 2
014672 PRELIMINARY: PRT: 748 AA.
AC 014672:
DT 01-JAN-1998 (TREMblrel. 05, Created)
DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE ADAM10.
CN ADAM10.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-974509925; PubMed-9305925;
RA Rosendahl M.S., Ko S.C., Long D.L., Brewer M.T., Rosenzweig B.,
RA Heil E., Anderson L., Pyle S.M., Moreland J., Meyers M.A., Kohno T.,
RA Lyons D., Lichenstein H.S.;
RT "Identification and characterization of a pro-tumor necrosis factor-
alpha-processing enzyme from the ADAM family of zinc
metalloproteases."

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RL J. Biol. Chem. 272:24588-24593(1997).
DR EMBL: AF009615; AAC51766.1; -.
DR HSSP: P18619; 1FVL.
DR InterPro: IPR001762; Disintegrin.
DR InterPro: IPR001590; Repolyisin.
DR InterPro: IPR000130; Zn_MTPeptide.
DR Pfam: PF00200; disintegrin.1.
DR Pfam: PF01421; Repolyisin.1.
DR SMART: SM00050; DISIN.1.
DR PROSITE: PS50215; ADAM_MPRO.1.
DR PROSITE: PS50214; DISINTEGRIN.2.1.
DR PROSITE: PS00142; ZINC_PROTEASE; UNKNOWN.1.
SQ SEQUENCE 748 AA; 84142 MW; 081E65B17022A71 CRC64;

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Query Match 96.0%; Score 3940.5; DB 4; Length 748;
Best Local Similarity 95.9%; Pred. No. 0;
Matches 718; Conservative 15; Mismatches 15; Indels 1; Gaps 1;

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QY 1 MVLPTVLLLSMAAGLGQGYGNPLNKYIRHYEGLSYVDSLHQKQRAKAVSHEDFL 60
Db 1 MVLPTVLLLSMAAGLGQGYGNPLNKYIRHYEGLSYVDSLHQKQRAKAVSHEDFL 60
QY 61 LLDFAHGRQPNLRMKRDTSLFSDFEKVEYSNKVLDYDTSHTYTGHIYGEESFSHGSVI 120
Db 61 LLDFAHGRQPNLRMKRDTSLFSDFEKVEYSNKVLDYDTSHTYTGHIYGEESFSHGSVI 120
QY 121 DGRFEGFIKTRGGTYIEPAERYIKDRLPHSHVYIHEDDINYPHKYPOGGCADHSVFE 180
Db 121 DGRFEGFIKTRGGTYIEPAERYIKDRLPHSHVYIHEDDINYPHKYPOGGCADHSVFE 180
QY 181 RMRKQMTGVEEGARAHBEKHAASGPELRRKRTTLAERNTCOLYIOTDHLFFKYGTR 240
Db 181 RMRKQMTGVEEGARAHBEKHAASGPELRRKRTTLAERNTCOLYIOTDHLFFKYGTR 240
QY 241 EAVIAQISSHYKALDTIYQTTDFSGIRNISFVKKRIRINTSDEKPTNPFPPNIGVEK 300
Db 241 EAVIAQISSHYKALDTIYQTTDFSGIRNISFVKKRIRINTSDEKPTNPFPPNIGVEK 300
QY 301 FLELNSEONHDDYCLAYVFTDRDGDVGLAWGAPSGSGGICEKSKLYSDGKKKSLN 360
Db 301 FLELNSEONHDDYCLAYVFTDRDGDVGLAWGAPSGSGGICEKSKLYSDGKKKSLN 360
QY 361 TGIITVQNGSHVPPKVSHTTFAHEVGNFSGPHDSGTECTPGEKSKNLGOKENGNTIWA 420
Db 361 TGIITVQNGSHVPPKVSHTTFAHEVGNFSGPHDSGTECTPGEKSKNLGOKENGNTIWA 420
QY 421 RATSQDKLNNNKFSLSIRINSQVLEKKRNCCFVESGPIGNGMVEQEGECDCGYSQD 480
Db 421 RATSQDKLNNNKFSLSIRINSQVLEKKRNCCFVESGPIGNGMVEQEGECDCGYSQD 480
QY 481 KDCCFPDANOPBGRKCKLPGKQCSPOGCTAOCFAKSKSEKCRDSDCAKEGICNGF 540
Db 481 KDCCFPDANOPBGRKCKLPGKQCSPOGCTAOCFAKSKSEKCRDSDCAKEGICNGF 540
QY 541 TALCPASDPKPRFTDCNRHTOVCLNGQAGSICEKYDLEBCTCASSDKDKNELCYVCCM 600
Db 541 TALCPASDPKPRFTDCNRHTOVCLNGQAGSICEKYDLEBCTCASSDKDKNELCYVCCM 600
QY 601 KMAPSTCAGTSGLOWSKQFSGRITTLQPGSPCNDPFGYCDVFMRCRLVDADGPLARLKK 660
Db 601 KMAPSTCAGTSGLOWSKQFSGRITTLQPGSPCNDPFGYCDVFMRCRLVDADGPLARLKK 660
QY 661 AIFSQLYENTIAEWIVAHMAVLLMGLALMLMAGFIKICSVHTPPSSNPKLPPPKPLPGT 720
Db 661 AIFSQLYENTIAEWIVAHMAVLLMGLALMLMAGFIKICSVHTPPSSNPKLPPPKPLPGT 720
QY 721 LKRRRPPQIPQORQRPRESYQMGHMR 749
Db 721 LKRRRPPQIPQORQRPRESYQMGHMR 749

RESULT 3

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Q10741  
ID Q10741 PRELIMINARY; PRT: 748 AA.  
AC Q10741;  
DT 01-NOV-1996 (Tremblrel. 01, Created)  
DT 01-NOV-1996 (Tremblrel. 01, last sequence update)  
DT 01-JUN-2001 (Tremblrel. 17, last annotation update)  
DE DISINTEGRIN-METALLOPROTEASE PRECURSOR (EC 3.4.24.-) (MYELIN-ASSOCIATED METALLOPROTEINASE) (MADM).  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovine; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
RC TISSUE-BRAIN;  
RX MEDLINE=96276398; PubMed=8694785;  
RA Howard L., Lu X., Mitchell S., Griffiths S., Glynn P.;  
RT "Molecular cloning of MADM: a catalytically active mammalian disintegrin-metalloprotease expressed in various cell types.";  
RL Biochem. J. 317:45-50(1996).  
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
CC -1- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN BRAIN. AT LOWER LEVELS IN KIDNEY, SPLEEN, LUNG AND HEART.  
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12C (ZINC METALLOPROTEASE).  
CC -1- SIMILARITY: HIGH, IN THE MIDDLE REGION, TO DISINTEGRINS.  
DR EMBL: Z21961; CAA79973.1; -.  
DR HSSP: P18619; 1FVL.  
DR MEROPS: M12.210; -.  
DR InterPro: IPR001762; Disintegrin.  
DR InterPro: IPR001590; Reprolysin.  
DR InterPro: IPR00130; Zn.MTpeptidase.  
DR Pfam: PF00200; disintegrin.1.  
DR Pfam: PF01421; Reprolysin.1.  
DR SMART: SM00050; DISIN.1.  
DR PROSITE: PS50215; ADAM\_MERPRO; 1.  
DR PROSITE: PS50214; DISINTEGRIN.2; 1.  
DR PROSITE: PS00142; ZINC\_PROTEASE; UNKNOWN.1.  
KM Disintegrin; Hydrolase; Metalloprotease; Transmembrane; Zinc; Signal;  
KW Glycoprotein.  
FT SIGNAL 1 19 POTENTIAL.  
FT PROPEP 20 213 POTENTIAL.  
FT CHAIN 214 455 METALLOPROTEINASE.  
FT CHAIN 456 550 DISINTEGRIN.  
FT DOMAIN 20 672 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 673 696 POTENTIAL.  
FT DOMAIN 697 748 CYTOPLASMIC (POTENTIAL).  
FT ACT\_SITE 384 384 BY SIMILARITY (BY SIMILARITY).  
FT METAL 383 383 ZINC (CATALYTIC) (BY SIMILARITY).  
FT METAL 387 387 ZINC (CATALYTIC) (BY SIMILARITY).  
FT METAL 393 393 ZINC (CATALYTIC) (BY SIMILARITY).  
FT CARBOHYD 267 267 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 278 278 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 439 439 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 551 551 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 748 AA: 84188 MW: 202E29830611F9E1 CRC64;

Query Match 94.7%; Score 3884.5; DB 6; Length 748;  
Best Local Similarity 94.4%; Pred. No. 0;  
Matches 707; Conservative 19; Mismatches 22; Indels 1; Gaps 1;

QY 1 MVLPTVILLLLSNAAGGGOYGNPLNKYTRHYEGLSNVYSLQKQKQARAVSHQOFL 60  
DB 1 MVLRLVILLLLSWAGGGOYGNPLNKYTRHYEGLSLVDLSLQKQKQARAVSHQOFL 60  
QY 61 LLDPFHANGROFNLMKRDSTLFSDEFKETSNNKVLDDYDTSHIYTGHIYGESEFSHGSYI 120  
DB 61 RLDPFHANGRFLNLMKRDSTLFSDEFKETSNNKVLDDYDTSHIYTGHIYGESEFSHGSYI 120  
QY 121 DGRREGFKRGFTYEPERIKIKRIIPHSVYIHEDDINYPHKYGGCAGDSHVPF 180  
DB 121 DGRREGFKRGFTYEPERIKIKRIIPHSVYIHEDDINYPHKYGGCAGDSHVPF 180

DB 121 DGRREGFKRGFTYEPERIKIKRIIPHSVYIHEDDINYPHKYGGCAGDSHVPF 180  
QY 181 RMKKYMTGVEEGARAHPEKHAASSPELLRRKRTTLARNTCOLYIOTDHLFFRYGTR 240  
DB 181 RMKKYMTGVEEGARAHPEKHAASSPELLRRKRTTLARNTCOLYIOTDHLFFRYGTR 239  
QY 241 EAVIAOISSHVKAIDITYTTPDSGIRNISFWKIRITNTSDEKOPTPPPPNIGVK 300  
DB 240 EAVIAOISSHVKAIDITYTTPDSGIRNISFWKIRITNTSDEKOPTPPPPNIGVK 299  
QY 301 FLELSEQNHDDYCLAYVFTDRDQDGLGLAWGAPSSSGGICEKSKLYSDGKKSLN 360  
DB 300 FLELSEQNHDDYCLAYVFTDRDQDGLGLAWGAPSSSGGICEKSKLYSDGKKSLN 359  
QY 361 TGIITVQNGSHVPPKVSHTTAHEVGNHFGSPHDSGTCTCTGESKNLQKENGNYIYA 420  
DB 360 TGIITVQNGSHVPPKVSHTTAHEVGNHFGSPHDSGTCTCTGESKNLQKENGNYIYA 419  
QY 421 RATSGBKLNKRNKSLCSIRNISQVLEKKRNCFVESGQPICGNGWEGEEDCGYSDQC 480  
DB 420 RATSGBKLNKRNKSLCSIRNISQVLEKKRNCFVESGQPICGNGWEGEEDCGYSDQC 479  
QY 481 KDDCEPDANQPEKCKKLPKQCSPOGPGCTAQCFAKSEKCKRSDSDCAKEGICNGF 540  
DB 480 KDDCEPDANQPEKCKKLPKQCSPOGPGCTAQCFAKSEKCKRSDSDCAKEGICNGI 539  
QY 541 TALCPASDPKPNFTDNRHTQVCINQCGASTICEKYLEECTCASSDGDKNELCHYCM 600  
DB 540 TALCPASDPKPNFTDNRHTQVCINQCGASTICEKYLEECTCASSDGDKNELCHYCM 599  
QY 601 KKAPASTCAGSTGSIQSKQFSGRTITLQSPGSPNDPRGCDYFMNRLVDADGPIARLKK 660  
DB 600 KKAPASTCAGSTGSIQSKQFSGRTITLQSPGSPNDPRGCDYFMNRLVDADGPIARLKK 659  
QY 661 AIFSPQLYENIAEWIAVAAVLMGIALIMLAGIKICSVHTPSSNKLPPPLPST 720  
DB 660 AIFSPQLYENIAEWIAVAAVLMGIALIMLAGIKICSVHTPSSNKLPPPLPST 719  
QY 721 LKRRRPPPIQPPRRPPRESYOMGMRR 749  
DB 720 LKRRRPPPIQPPRRPPRESYOMGMRR 748

RESULT 4  
Q10742 PRELIMINARY; PRT: 691 AA.  
ID Q10742;  
AC Q10742; Q92650;  
DT 01-NOV-1996 (Tremblrel. 01, Created)  
DT 01-NOV-1996 (Tremblrel. 05, last sequence update)  
DT 01-JUN-2001 (Tremblrel. 17, last annotation update)  
DE DISINTEGRIN-METALLOPROTEASE MADM (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC MEDLINE=96276398; PubMed=8694785;  
RA Howard L., Lu X., Mitchell S., Griffiths S., Glynn P.;  
RT "Molecular cloning of MADM: a catalytically active mammalian disintegrin-metalloprotease expressed in various cell types.";  
RL Biochem. J. 317:45-50(1996).  
DR EMBL: Z48579; CAA8463.1; -.  
DR HSSP: P18619; 1FVL.  
DR MEROPS: M12.210; -.  
DR InterPro: IPR001762; Disintegrin.  
DR InterPro: IPR001590; Reprolysin.  
DR InterPro: IPR00130; Zn.MTpeptidase.  
DR Pfam: PF00200; disintegrin.1.  
DR Pfam: PF01421; Reprolysin.1.  
DR PRINTS: PR00289; DISINTEGRIN.  
DR SMART: SM00050; DISIN.1.  
DR PROSITE: PS50215; ADAM\_MERPRO; 1.

DR PROSITE; PS50214; DISINTEGRIN\_2; 1.  
 DR PROSITE; PS00142; ZINC\_PROTEASE; UNKNOWN\_1.  
 KW INTEGRIN.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 691 AA; 77632 MW; 8843698F24BB292 CRC64;

Query Match 81.6%; Score 3346; DB 4; Length 691;  
 Best Local Similarity 88.4%; Pred. No. 4.5e-264;  
 Matches 612; Conservative 16; Mismatches 12; Indels 52; Gaps 2;

109 GREGSGVSDGDEGEEFGITRGSTFIEPAERIKRILPHSVYIHEDIN----- 162  
 1 GEGSFGSGVSDGDEGEEFGITRGSTFIEPAERIKRILPHSVYIHEDISERLKL 60  
 163 -----YPRKYPGGCADHS 177  
 61 LRLKLSLEMTSCCLPCLALLSHMKKAVNSHCLYFKDQWGESEIYPIKYPGGCADHS 120  
 178 VFERMKYQMTGVEGARAHPEKHAASGPELLRRKRTTLAERNTCOLYIQTDHLEFKY 237  
 121 VFERMKYQMTGVEEVTOIQDEHAA-NGPELLRRKRTTSAEKNKCOLYIQTDHLEFKY 179  
 238 GTRAVINQISHVKAIDITTYQTDFSGIRINSEWKRIRINTSDKEDPTNPREPNI 297  
 180 GTRAVINQISHVKAIDITTYQTDFSGIRINSEWKRIRINTADEKPTNPREPNI 239  
 298 VEKFLSESNHNDYCLAYFTDRFDGVLGLWVAPSGSGGICEKSKIVSDGKK 357  
 240 VEKFLSESNHNDYCLAYFTDRFDGVLGLWVAPSGSGGICEKSKIVSDGKK 299  
 358 SLNTGIIIVQYNGSHVPRKVSHTTPAHEVGHFSGPHDSGTECPGSEKNLQKENGNY 417  
 300 SLNTGIIIVQYNGSHVPRKVSHTTPAHEVGHFSGPHDSGTECPGSEKNLQKENGNY 359  
 418 MYARATSGDKLNKNSFSLSTRINISQVLEKRRNCFVSSGPIGNGVVEGEECDGYS 477  
 360 MYARATSGDKLNKNSFSLSTRINISQVLEKRRNCFVSSGPIGNGVVEGEECDGYS 419  
 478 DOCKDCCFDANQPEGKCKLKPQKCSPSGPGCTAACAFKSKSEKRDSDCAKEGIC 537  
 420 DOCKDCCFDANQPEGKCKLKPQKCSPSGPGCTAACAFKSKSEKRDSDCAKEGIC 479  
 538 NGFTALCPASDPKPNFTDCNRHTQVINGOCAGSICEKYDELECTCASSDGKNKELCHV 597  
 480 NGFTALCPASDPKPNFTDCNRHTQVINGOCAGSICEKYDELECTCASSDGKNKELCHV 539  
 598 CCMKMASTGASTGSLMSKOFSGRTTTLQPSGPNDFRGYCFVEMCRVLVDADGLAR 657  
 540 CCMKMASTGASTGSLMSKOFSGRTTTLQPSGPNDFRGYCFVEMCRVLVDADGLAR 599  
 658 LKKAIFSPOLYENIAEWIVAHMAVLLMGIALIMAGFICGSVHTPSSNPKLPPPKPL 717  
 600 LKKAIFSPOLYENIAEWIVAHMAVLLMGIALIMAGFICGSVHTPSSNPKLPPPKPL 659  
 718 PGTLLRRRRPQIPQPRQPRPRESTQMGHMR 749  
 660 PGTLLRRRRPQIPQPRQPRPRESTQMGHMR 691

RESULT 5  
 Q10743 PRELIMINARY; PRT; 544 AA.  
 AC Q10743;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)  
 DE DISINTEGRIN-METALLOPROTEINASE PRECURSOR (EC 3.4.24.-) (MYELIN-ASSOCIATED METALLOPROTEINASE) (MAM) (FRAGMENT).  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 NCBI\_TaxID=10116;

11  
 RN SEQUENCE FROM N.A.  
 RP STRAIN-SPRAGUE-DAWLEY; TISSUE=BRAIN;  
 RX MEDLINE=96276398; Pubmed=8694785;  
 RA Howard L., Mitchell S., Lu X., Griffiths S., Glynn P.;  
 RT "Molecular cloning of MAM: a catalytically active mammalian  
 RT disintegrin-metalloprotease expressed in various cell types";  
 RL Biochem. J. 317:45-50(1996).  
 CC 1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
 CC 1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B (ZINC  
 CC METALLOPROTEINASE); ALSO KNOWN AS THE REPROLYSIN SUBFAMILY.  
 CC 1- SIMILARITY: HIGH, IN THE MIDDLE REGION, TO DISINTEGRINS.  
 DR EMBL; Z46444; CAAB6359.1; ..  
 DR HSSP; P18619; 1FVU.  
 DR MEROPS; M12.210; ..  
 DR InterPro: IPR001762; Disintegrin.  
 DR InterPro: IPR001590; Reprolysin.  
 DR InterPro: IPR000130; Zn\_MTPeptide.  
 DR Pfam; Pf00200; disintegrin; 1.  
 DR Pfam; Pf01421; Reprolysin; 1.  
 DR PRINTS; PR00289; DISINTEGRIN.  
 DR SMART; SM00050; DISIN. 1.  
 DR PROSITE; PS50215; ADAM\_MEROPS; 1.  
 DR PROSITE; PS50214; DISINTEGRIN\_2; 1.  
 DR PROSITE; PS00142; ZINC\_PROTEASE; UNKNOWN\_1.  
 KW Integrin; Hydrolase; Metalloprotease; Transmembrane; Zinc; Signal;  
 KM Glycoprotein.  
 FT NON\_TER 1 1  
 FT SIGNAL <1 9  
 FT CHAIN 10 241 METALLOPROTEINASE.  
 FT CHAIN 242 346 DISINTEGRIN.  
 FT DOMAIN 10 468 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 469 492 POTENTIAL.  
 FT DOMAIN 493 544 CYTOPLASMIC (POTENTIAL).  
 FT ACT SITE 180 180 BY SIMILARITY.  
 FT METAL 179 179 ZINC (CATALYTIC) (BY SIMILARITY).  
 FT METAL 183 183 ZINC (CATALYTIC) (BY SIMILARITY).  
 FT METAL 189 189 ZINC (CATALYTIC) (BY SIMILARITY).  
 FT CARBOHYD 63 63 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 74 74 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 235 235 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 347 347 N-LINKED (GLCNAC...) (POTENTIAL).  
 SQ SEQUENCE 544 AA; 60444 MW; F75E0EBD6C8BA7DD CRC64;

Query Match 72.0%; Score 2956; DB 11; Length 544;  
 Best Local Similarity 98.5%; Pred. No. 1.9e-232;  
 Matches 536; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

206 GPELLRRKRTTLAERNTCOLYIQTDHLEFKYGTREAVINQISSHVKAIDITTYQTDFSG 265  
 1 GPELLRRKRTTLAERNTCOLYIQTDHLEFKYGTREAVINQISSHVKAIDITTYQTDFSG 60  
 266 IRLNSEWVKRIRINTSDKEDPTNPREPNIQVEKFLSESNHNDYCLAYFTDRFD 325  
 61 IRLNSEWVKRIRINTSDKEDPTNPREPNIQVEKFLSESNHNDYCLAYFTDRFD 120  
 326 DGVYGLWVAPSGSGGICEKSKLYSDGKKSLNTGIIIVQYNGSHVPRKVSHTFAHE 385  
 121 DGVYGLWVAPSGSGGICEKSKLYSDGKKSLNTGIIIVQYNGSHVPRKVSHTFAHE 180  
 386 VGNHFGSPHDSGTECPGSEKNLQKENGNYIMYARATSGDKLNKNSFSLSTRINSQVL 445  
 181 VGNHFGSPHDSGTECPGSEKNLQKENGNYIMYARATSGDKLNKNSFSLSTRINSQVL 240  
 446 EKKRNKCFVSSGPIGNGVVEGEECDGYSPOCKDCCFDANQPEGKCKLKPQKCS 505  
 241 EKKRNKCFVSSGPIGNGVVEGEECDGYSPOCKDCCFDANQPEGKCKLKPQKCS 300  
 506 PSOGPGCTAACAFKSKSEKRDSDCAKEGICNGFTALCPASDPKPNFTDCNRHTQVCIN 565  
 301 PSOGPGCTAACAFKSKSEKRDSDCAKEGICNGFTALCPASDPKPNFTDCNRHTQVCIN 360

QY 566 GGCAGSICEKYDELECTCTCASSDCKDNKELCHVCCMKMAPSTCAGSLQWSKQFSGRTI 625  
 DB 361 GGCAGSICEKYDELECTCTCASSDCKDNKELCHVCCMKMAPSTCAGSLQWSKQFSGRTI 420  
 QY 626 TTAGSPCNDPFGYCVFRCRCLYDADGPLARLKAIFSPQLENTIAEIVAHMAVLLM 685  
 DB 421 TTAGSPCNDPFGYCVFRCRCLYDADGPLARLKAIFSPQLENTIAEIVAHMAVLLM 480  
 QY 686 GIALIMMAGFKICSVHPPSSNPKLPKPLPGTLKRRRPPQIQPPROPRESYONG 745  
 DB 481 GIALIMMAGFKICSVHPPSSNPKLPKPLPGTLKRRRPPQIQPPROPRESYONG 540  
 QY 746 HMR 749  
 DB 541 HMR 544  
 RESULT 6  
 QYVJW9 PRELIMINARY; PRT: 1238 AA.  
 AC QYVJW9: 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE KUZ PROTEIN.  
 GN KUZ OR BG:DS07660.3 OR CG7147.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 NC NCB1\_Taxid=7227;  
 RX STRAIN=BERKELEY.  
 RC MEDLINE=20196006; PubMed-10731132.  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle J.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blaise R.G., Champagne M., Pfeiffer B.D.,  
 RA Abail J.F., Abdoulaye A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Bernier B.P., Bhandari D., Bolshakov S.,  
 RA Borovka D., Botchan M.R., Bouck J., Brockstein P., Brotlier P.,  
 RA Burlis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup I.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Fertler S., Fleischmann W.,  
 RA Foster C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,  
 RA Glodok A., Gong F., Gorell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jaitli M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodish C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Laso P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Matel B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclib J.M.,  
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reibert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Slier E., Spredling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weisslock G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,  
 RT "The genome sequence of Drosophila melanogaster.";  
 RL Science 287:2185-2195(2000).

DR EMBL: AE003640; AAF53318.1; -  
 DR HSSP: P17494; 1KST.  
 DR Flybase: FBgn0015954; Kuz.  
 DR InterPro: IPR001672; Disintegrin.  
 DR InterPro: IPR001590; Kepralysin.  
 DR InterPro: IPR000130; Zn\_MTEPde.  
 DR SMART: SM00050; DISIN; 1.  
 DR PROSITE: PS00215; ADAM\_MEPPO; 1.  
 DR PROSITE: PS00214; DISINTEGRIN; 2; 1.  
 DR PROSITE: PS00442; ZINC\_PROTEASE; UNKNOWN\_1.  
 DR SEQUENCE 1238 AA; 136407 MW; 960924B618AC472 CRC64;

Query Match 36.3%; Score 1489.5; DB 5; Length 1238;  
 Best Local Similarity 34.4%; Pred. No. 1.7e-112;  
 Matches 337; Conservative 131; Mismatches 267; Indels 245; Gaps 22;

QY 7 LILLMAAGLG-QYGNP-LNKYIRHGYGLSYNDVSLHOKHOKRAVSHEDQFLDLE 64  
 DB 17 LIIYVYAKDISGVKRGHERLNEYISHYETLNYDHEHIRASHNRRARSVT-KDQYVHLKF 75  
 QY 65 HAHGQFNIIRAKRDTSLSDSEKVTSTKXVLDYDTSHIYTHIYEGSGSHGYIDGRF 124  
 DB 76 ASHGDFHLRLKRLNFTSNKLDIFYDSKPIDYSTDHIYEGFVIGDRNSYVFGSIHNGVF 135  
 QY 125 EGFITRGSTFYIEPAERYI----- 144  
 DB 136 EKITTEDAYVEAHAKHYFPNRTATTPPTSTSTSSATTAATNSYQTPRLANSMTST 195  
 QY 145 -----KDR-----ILPHS 153  
 DB 196 AVNSKTEPNFKIKIASSTTSQQLPEYTESSSSTTPPTTEFEDEKERNABDELPHS 255  
 QY 154 VLY---HEDDINYPKYPQSGCA-----DHSVFERMRK 184  
 DB 256 ILYKSHEDAVENREHVAACGTTDEVSOEMENIQNSAVEELPEPMKDYOKLHRKL 315  
 QY 185 YQMTVEEGARAPHKNAASSG-----PELLRKRKTTAE----- 219  
 DB 316 HKSAPOOQOQHPKKYISGDEDEKYPHOKYTKANAEAGAFYDPSGRLLGSSANVAD 375  
 QY 220 -----RNTCOLYIOTDLHPKY----- 237  
 DB 376 WHQLVHERVRATONGADDRSGSGRGREDNKKTCGLYIQTDLIRHIREGIAHODR 435  
 QY 238 -----GTRAVYAOISSHYKAIIDTYIQTDSG---INISFMVKRIINTS--- 282  
 DB 436 GRKYEVDEKTRREITSLAHHTAVANYIYRNKTFEGRTREHNRIFREYORIKRIDDSACRN 495  
 QY 283 DEKDTNFRFPNIGVEKFELENSQNHDDYCLAVFTDRPDGVLGAWAGAPSGSSG 342  
 DB 496 SYNGHNAFCNEMHVSNFLNLSLSDHSDCLAVFYFRPTGTGLGLAWAVASGASG 555  
 QY 343 GICEKSKLYSD-----GKKSLNTGITTYQNGSHVPPVSHITFAHEVGHNGSPHD 395  
 DB 556 GICEKFKYTYETVGGQYSTKRLSLTGTITFVNVSRRPVVSOQLLAHELIGHNGSPHD 615  
 QY 396 SGTETPESKRLGCKENGNTIYARATSCDKLNNKSLCSIRINISYLE-----KRRNN 451  
 DB 616 YPQECRPGCL-----NGNYIMFASATSGDRPNNSKSPSIRINISVLDVLVGNKRD 668  
 QY 452 CFVEGQPIICGNGWGEQECDCGYS-DQCKDDCCF-----DANGPECKKCLKGK 502  
 DB 669 CFKASGAFPCGKIKYTESSEEDCCGNEEDCKCIPPLIETDOSLNSKAKGCTRRAKT 728  
 QY 503 QCSPPGQPCCTA-QCAF--KSKSEKCRDSDCAKGLCNGFTALCPASDPKPNFTDCNRH 559  
 DB 729 QCSPPGQPCCTA-SCTFVPSYHVKCKRETECSMSNGTGTACCPERRHDDTWCNG 788  
 QY 580 TQVCGAGCAGSICEKYDELECTCTCASSDCKDNKELCHVCCMKMAPSTCAGSLQWS 617  
 DB 789 TALCIRGECSSGPELLMNMTRCFLTSTPLPHVYSRRKLCIDLACODGNDPTSTCRSTSEPADK 848

QY	618	KQFSRTTIDLPQSGCNDPFGCYDVFMRCCRYADADGPIARLKKALFSPOLVENIAEWIYA	677
Db	849	YNIQKGGTSLDPGSCDNPFGCYDVFMRCCRYADADGPIARLKKALINKTKTLQTVAEWIVD	908
QY	678	HWMAVLLMGIALIMLMAFGIKCYVHPDSSNPKLPPLPGLTKL-----RRRPPQIQ	731
Db	909	NMYLVLVLMGVAFIVYMGSEFIKCAAVHTPSSNPKRRRRARRISSETLRAPMNTLRRMRQHPNQ	968
QY	732	Q--PPRRPRESYOGCHMR	749
Db	969	KGACPRSTIPPAHNAQHTSR	988
RESULT	7		
ID	094902	PRELIMINARY;	PRT; 1239 AA.
AC	094902;		
DT	01-FEB-1997	(TREMBLrel. 02, Created)	
DT	01-FEB-1997	(TREMBLrel. 02, Last sequence update)	
DT	01-JUN-2001	(TREMBLrel. 17, Last annotation update)	
DE	KUZBANIAN.		
GN	KUZ OR BG:DS07660.3 OR CG7147.		
OS	Drosophila melanogaster (Fruit fly).		
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;		
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;		
OC	Ephydroidea; Drosophilidae; Drosophila.		
OX	NCBI_TaxID=7227;		
RN	(1)		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=96355647; PubMed=8703057;		
RA	Rooke J., Pan D., Xu T., Rubin G.M.;		
RT	"KUZ, a conserved metalloprotease-disintegrin protein with two roles		
RT	in Drosophila neurogenesis."		
RL	Science 273:1227-1231(1996).		
DR	EMBL; U60591; AAC47275.1; "		
DR	HSSP; P17494; 1KST.		
DR	MEROPS; M12.211; "		
DR	Flybase; FBgn0015954; kuz.		
DR	InterPro; IPR001762; DisIntegrin.		
DR	InterPro; IPR001590; Reprolysin.		
DR	InterPro; IPR000130; Zn_MTPeptide.		
DR	SMART; SM00050; DISIN; 1.		
DR	PROSITE; PSS0215; ADAM_MEPRO; 1.		
DR	PROSITE; PSS0214; DISINTEGRIN; 1.		
DR	PROSITE; PSS00142; ZINC_PROTEASE; UNKNOWN_1.		
KW	Neurogenesis;		
QO	SEQUENCE 1239 AA; 136522 MW; 7FCB51A1A1352577A CRC64;		

Query Match	36.3%	Score 1489	DB 5	Length 1239
Best Local Similarity	34.4%	Pred. No. 1.9e-112		
Matches 337	Conservative 131	Mismatches 267	Indels 246	Gaps 22

[illegible]

QY	184	KYOMTGEESGARHAEKHAASSG-----PELLRKKPTTLE-----	219
Db	316	LHKSAPFOQQQPHPPKKYISGDEDFEYPRUKYTKENAPFEGAFEDPSTORLIGSSANVA	375
QY	220	-----RNTCOLYIQTDLHFEFY-----	237
Db	376	DMHOLVHERVRRATDNCAGDSSGSGRGREDNRKNNIYIOTDPLMRHIREGIADHD	435
QY	238	-----GPRELVIAOISSHWVAIDTITYOTDFSG-----IRNSFWVRKIRINTNS---	282
Db	436	RGRKYEYDEKTRBITSLAHNHYAIVYIRNTRKFDERTHRNTRREYQVAKIDDDSACR	495
QY	283	-DEKDPTNPERFPPIGYEKEFLTLESDONHDYCLAVYFTDRDEDDVGLGAWAPSGSS	341
Db	496	NSYGNPHAFNCENHMDVSNFNLTLSTLHDSHDFCLAVYFTYRDFGTLGLAWASAGAS	555
QY	342	GGTEKSKLYSD-----GKKKSLNGIITVQNYGSHVAPPKSHITFAIEVGHNGSPH	394
Db	556	GGICEKTKYTYETVGGYOYOSTRSLNGIITFVYNSRVPPKSOQLTALHAEIGHNPSPH	615
QY	395	DSGTECTPGESKNLGOKENGYIYARATSGDKLNKKFSLCSIRNTSOYLE----KRN	450
Db	616	DYPECCRGGL-----NGMYIFASATISGDRNNNSKFEPCSRINSNVLDVLYGNTR	668
QY	451	NCYVESGOPITGNGMVEDEGCCDGYG--DOCKDDCGF-----DANOPEGKKKILPG	501
Db	669	DCFPASBEAFPCGNKTVSGECCDCGFNEDECKKCCYPRLTSEYDOSLANSAGCTPRRAK	728
QY	502	KCGSPSOCPCTA-QCAF--KSKSECRDSDCAKEGJNGFTALCPASDPKPNFTPCNR	558
Db	729	TQCSFSQCPCLSNSTCFVPISTYQKKKELEFCMSNSTCGTTARECEPRHRDRTKCN	788
QY	559	HTQVCINCQAGSICKEYDLEEC--TCASSDGKDKELCHVCCMKKMASTCASTGSLQW	616
Db	789	GTALCIRCEQSGPCLLMMNTKCLFTTLPVHSRKILCLADODGNDTSTCRSTSEFAD	848
QY	617	SKQSPGRITLQSPSPONDPCGYADVYMBRCIYNADQPLARIKKAIJPSQLYENIMAVY	676
Db	849	KYNTQKGISLQPSPCDNFGYQDVFLKCAVADADQPLRLTKKLLNKRKTLDTQVWEMY	908
QY	677	AHMAVILMGTALMLNAGFLTKISVHTPSSNPKLPKPKLPGLT-----RRRPOP	730
Db	909	DNMYLTVLWGAFAIVYMGSFKCCAVHTPSSNPKRRARRISETLRAPMNTLRBMQHNP	968
QY	731	QO--PPQRAPRESYONGHMRR	749
Db	969	QRGACPRISIPPAHEADQHSYR	989

Q9NKF9	RESULT	8
ID	Q9NKF9	PRELIMINARY; PRT; 1236 AA.
AC	Q9NKF9;	
DT	01-OCT-2000 (TREMBLrel. 15, Created)	
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)	
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)	
DE	KUZ PROTEIN.	
CN	KUZ OR BG:DS07660.3 OR CG7147.	
OS	Drosophila melanogaster (Fruit fly).	
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;	
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;	
OC	Ephydroidea; Drosophilidae; Drosophila.	
OX	NCBI_TaxId=7227;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=Y, CN BW SP.	
RA	MEDLINE=99403001; PubMed=10471707;	
RA	Asbunner M., Misra S., Roote J., Lewis S.E., Blazej R., Davis T.,	
RA	Doyle C., Galle R., George R., Harris N., Hartzill G., Harvey D.,	
RA	Hong L., Houston K., Hoskins R., Johnson G., Martin C., Moshrefi A.,	
RA	Palazzo M., Reese M.G., Spadling A., Tsang G., Wan K., Whitelaw K.,	
RA	Celniker S., Rubin G.M.;	
FT	"An exploration of the sequence of a 2.9-Mb region of the genome of	











Best Local Similarity 25.4%; Pred. No. 2,6e-25;  
Matches 165; Conservative 98; Mismatches 263; Indels 123; Gaps 34;

QY 9 LLSW--AALG--OYGNPLNKYIHRHYEGLSYNDLSQKQORAKRAVSHEDOFLLD 63  
DB 12 LRLRWLACGLLGLVLEAGRPDLLEQVHLS--SYEITTPRLTRERREALGPSQOISY 69  
QY 64 FNAHQFNLKMRDTSLSFDEKFEVTSNK---VLDDYD--SHI-YTHGYEGSGFSH 116  
DB 70 IQAGKOHILHLEIRNTDLLPNDVYVYTYDEKGLSDHPVQSHCHYRGVEGVQNSAVA 129  
QY 117 GSYIDRFEGEFTIRGTFYIEPAERYIKDRLLPHSVIYHEDDIWPKHYGCGCADA 176  
DB 130 VSAFCG--LRGLHLNNAFGEIPLNNSH---FEHIFPMGI---HOEPLRCGVSNR 180  
QY 177 SVFERMKYOMTVEGASRAHPEKHAASGPELLRRKRTTLARNICOLYIOTDHLFFKY 236  
DB 181 DT-----EKSTQODEEH--PSYQLRRRAALPOTRYVELFTYVDKERIDM 227  
QY 237 YGTRE-AVIAQISSHVKAIDTYQTDFSGIRNISPMVKRIRINTTSDEKPTNPRFPN 295  
DB 228 MGRNQTAVREEMIRLANLYDSMT-----MLNRIYLVGLEIWT---DRNPINIGAG 278  
QY 296 IGEKFLF-----LNSQNHDDYCLAVFTDRDDGVGLAWGAPSGSGGICEKSKL 350  
DB 279 DVIGNFPQMRKFLITRRHDS---AQLVLKGF--GGTAGMAFVG-----VCSRS-- 325  
QY 351 YSDGKKSLNT--GIITYQNGSHVPPKVSHTIPAHEVGHFSGPHSGTECPGEEKNLG 409  
DB 326 HAGG---INVFOIYVERPASIY-----AHELGHNLGNHDDGRCEFCAG-- 368  
QY 410 QKENGNTIYARATSGDKLNKNSFLCSIRNISQVLEKRNCFE-----SGQPIG 462  
DB 369 -----SCINSGAS-----GSRNFSASADEFKLTINKGSCLLNIPKDEAYSPSG 418  
QY 463 NGAVEGECDDGYSDQCK--DCCFDANQDEGKKKLPKQCSPOGECTACQAFKSK 521  
DB 419 NKLVDPGEEDCGTAKCEVDPC-----EGSTCKLKSAEC--AYGDC--KDCQFLRG 469  
QY 522 SEKCR--DSDCAKEGICNGFTALCPASDPKPNFTDCNRHTQVINCAGASICEKDL 580  
DB 470 GSMCRGTSCEVDYPCNGSGSPCPDVFIONGYPCQNSKATYNG-----MGQYIDAQ-- 523  
QY 581 CTASASDGDKNELCHVCCMKKAP---STCSTGSLQMSKQFSRTI 625  
DB 524 --COVIFGSKAKAPRDCFEVNSKGRGNCJSGS--EYKCATGNAL 569

RESULT 14  
Q9PVK7 PRELIMINARY; PRT; 600 AA.  
AC Q9PVK7;  
DT 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
DE COBRIN PRECURSOR.  
OS Naja naja (Indian cobra).  
OC Naja naja; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
OC Elapidae; Elapinae; Naja.  
OX NCBI\_TaxID=35670;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-KAOUTHIA; TISSUE-VENOM GLAND;  
RA Bamba B., Bredenhorst R., Vogel C.-W.;  
RL Submitted (MAY-1998) to the EMBL/Genbank/DBJ databases.  
DR HSP; P17494; 1KST.  
DR InterPro: IPR001162; Disintegrin.  
DR InterPro: IPR002870; Pep\_M12B\_propep.  
DR InterPro: IPR001590; Reprolysin.  
DR InterPro: IPR000130; Zn\_MTPeptidase.  
DR Pfam; PF00200; disintegrin; 1.

DR Pfam; PF01562; Pep\_M12B\_propep; 1.  
DR Pfam; PF01421; Reprolysin; 1.  
DR PRINTS; PR00289; Disintegrin.  
DR Prodbm; PD000664; Disintegrin; 1.  
DR SMART; SM00050; Disin; 1.  
DR PROSITE; PS50215; ADAM\_MEPRO; 1.  
DR PROSITE; PS50214; Disintegrin\_2; 1.  
DR PROSITE; PS00142; ZINC\_PROTEASE; UNKNOWN\_1.  
KW Signal.  
FT SIGNAL 1 6 POTENTIAL.  
FT CHAIN 180 600 COBRIN.  
SQ SEQUENCE 600 AA; 67661 MW; C7C0D45EBC694290 CRC64;

Query Match 10.0%; Score 409; DB 13; Length 600;  
Best Local Similarity 24.1%; Pred. No. 6,8e-25;  
Matches 156; Conservative 97; Mismatches 236; Indels 156; Gaps 31;

QY 47 QRAKRAVSHEDOFLLDFAHGRNFLRMRDTSLSFDEF-----KVEYSNKYLD 96  
DB 36 QNPQPEYKEDT--MVEFQVNGEPVLIHLERKGLFSEDTETHYAPDGRREITTSPPVD 94  
QY 97 YDTHIYTHIYEGESFSGSVIDGREGFTKTGTFYIEPAERYIKDRLLPHSVIY 156  
DB 95 H---CYHGYFQNEADSSAVISACDG--LKGHPKLGELIETIEPLK--ISDS--EANA--IY 145  
QY 157 HEDDINYPKHYGPOGCGADSHVEERMKYOMTVEEGARAHPEKHAASGPELLAKKRTT 216  
DB 146 KDNVEEDEDPTKIGYVD--TWESDEPKTSL-----LNTPE--QDRTL 189  
QY 217 LAERNICQYIOTDHLFFKYGTREAVI--AQISSHVKAIDTYQTDFSGIRNISPMVKR 275  
DB 190 QAEK-YIEFYAVVDNIMVHYKRNQVYIKRKYEMINIMMYIRLNF-----HILJGLE 244  
QY 276 I-----RITPTDEKOPTNPERFNPINIGVEKLELNSQNHDDYCLAVFTDRDDGVLG 330  
DB 245 IMSNINEIWNQSDVATDLDL-----GEWEKRLLPKRRKND--AQLITGIDFNGTFVG 296  
QY 331 LAMVGAPSGSSGICEKSKLYSDGKKSLNTGIIIVQNGSHVPPKVSHTIPAHEVGHNF 390  
DB 297 LAVIGS-----ICNP-----KTSAAVQDYSKT--RMAVITMAHEMGNL 335  
QY 391 GSPHDSGTECTPGESKNLQKENGNTIYARATSGDKLNKNSFLCSIRNISQVLEKRN 450  
DB 336 GNMHDKGF--CTCGFMK-----CVMSTRTK---PAYQFSSCSVREHORYLLDRP 381  
QY 451 NCFVES-----GQPIGNGVYEGEEDCGYSDQCKDDCCFDANQDEGKKKLPKQ 503  
DB 382 QCLINKPLSTDIVSPPTGNYFEVEGECDCGSPADCSACC-----NATTCRLQHEAQ 435  
QY 504 CSPSOGPCTACQAFKSKSEKCR--DSDCAKEGICNGFTALCPASDPKPNFTDCNRHTOV 562  
DB 436 CQSE---CEKCKKKGAGABEAKAKDDCDLPELCTGSASCEPTVFORNGLPC--QNNGY 491  
QY 563 CTNGCC-----AGSICEKYDLEECTCASSDGKDK 592  
DB 492 CYNGKCPINTNOCIALRPGVAVSRDSCFTLNQPTRGGLCIMEYGRKIPCAAKVQKGR 551  
QY 593 ELG-----HYCCMKKAPSTGASTGSLQMSKQFSRTITLQSGSPND 635  
DB 552 LFCKRRNSMICSTISPRD--PSYG-----WVEGTKGCD 584

RESULT 15  
Q77633 PRELIMINARY; PRT; 75 AA.  
AC Q77633;  
DT 01-NOV-1998 (Tremblrel. 08, Created)  
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)  
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
DE DISINTEGRIN-METALLOPROTEINASE PRECURSOR (FRAGMENT).  
GN ADAM-10.  
OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Flannery C.R., Little C.B., Caterson B., Hughes C.E.;  
 RT "Expression of articular cartilage metalloproteinases by chondrocytes  
 in fresh tissue and explant, monolayer and agarose cultures.";  
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF069645; AAC23529.1; -  
 DR MEROPS; M12.210; -  
 DR InterPro; IPR01590; Reprolysin.  
 DR PROSITE; PS50215; ADAM\_MEPRO; 1.  
 KW Integrin.  
 FT NON\_TER 1 1  
 FT NON\_TER 75 75  
 SO SEQUENCE 75 AA; 8224 MW; C03B70C901333557 CRC64;

Query Match 9.9%; Score 406; DB 6; Length 75;  
 Best Local Similarity 100.0%; Pred. No. 7.3e-26;  
 Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 393 PHDSGTCTPESKNILOKENGNYIMYARATSGDKLNKFKSLCSIRNISQVLEKRRNC 452  
 |||||  
 Db 1 PHDSGTCTPESKNILOKENGNYIMYARATSGDKLNKFKSLCSIRNISQVLEKRRNC 60  
 OY 453 FVESGQPIGNGWVE 467  
 |||||  
 Db 61 FVESGQPIGNGWVE 75

Search completed: April 1, 2002, 15:12:14  
 Job time: 696 sec